

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 9, 2001, 23:31:06 ; Search time 2385.2 Seconds
(Without alignments)
8715.686 Million cell updates/sec

Title: US-09-670-568B-2_COPY_145_1488
Sequence: 1 atgtcccgagcacacagac.....caaacgatacgttaccaca 1344

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba1: *
2: gb_ba2: *
3: gb_ba3: *
4: gb_in1: *
5: gb_in2: *
6: gb_in3: *
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12: gb_pl1: *
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15: gb_pl4: *
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17: em_ba2: *
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20: em_higo_inv: *
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97: gb_pr10: *
98: em_ba3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1344	100.0	1347	88 AF075428	AF075428 Homo sapi
2	1344	100.0	2816	85 AB016072	AB016072 Homo sapi
3	1232	91.7	1351	88 AF075432	AF075432 Homo sapi
4	1232	91.7	1926	88 AF075430	AF075430 Homo sapi
5	1232	91.7	2031	89 AF116771	AF116771 Homo sapi
6	1232	91.7	2270	85 AB016073	AB016073 Homo sapi
7	1232	91.7	4846	9 AX009538	AX009538 Sequence
8	1232	91.7	4849	92 HSA16961	Y16961 Homo sapien

Query Match	Best Local Similarity	Matches 1344; Conservative	100.0%; Score 1344; DB 88; Length 1347; 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1	ATBTCCCAAGAGCACACAGACAANAATGATATTCCTCAAGTCCAGAGGTTTCCAGCATATTCGG 60		
QY 61	gatcttcctggnaacagcctataatgttcagttcagttcagcccatatgacttgtaacttgttgatgaa 120	61	gatcttcctggnaacagcctataatgttcagttcagttcagcccatatgacttgtaacttgttgatgaa 120
DB 61	GATTTTCTGTGACACGCCCTATATGTTTCAGTTCAGGCCCATGACTTGAACCTTTGTGATGAA 120		
QY 121	ccatcagaagaatggtgcgcgaacaagaatttgatgatatgaatgagactgtatccgaatgcag 180	121	ccatcagaagaatggtgcgcgaacaagaatttgatgatatgaatgagactgtatccgaatgcag 180
DB 121	CCATTCAGAAAGATGGTGTGCACAAACAGATGTGAGATTACATGACATGACTATCTCCGATCGAG 180		
QY 181	gactcggacctgagtgaaccctatctggccacagtatcacgaaccttggggctctcttgaacgc 240	181	gactcggacctgagtgaaccctatctggccacagtatcacgaaccttggggctctcttgaacgc 240
DB 181	GACTCGGACCTGAGTGAACCCCATGTGTGGCCACAGATACACGAACCTGGGGCTCTCTTAACAGC 240		

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Oy 781 acgacagctctgtacaaattcattcatgttgaacagcagttgttggaggatgaaccgacct 840
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Db 841 CCAATTTATTCATTTGTACTCTGTGAAACACAGAGATGGCAAGTCCGTGGGCGACGCTGC 900
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Db 901 TTTGAGGCCCCGGATCTGTCTGTGCCAGGAAGACAGAAAGCGGATGGAAGATGACATC 960
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Db 961 AGAAGAGCAGAGTTTGGACAGTACAAAGACGGTATGATGGAAGCGCGCTTTCGT 1020
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Db 1021 CAGAACACATGATGTATCCAGATGACATCCATCAAGAAAGAAAGATCCCATGATGAA 1080
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RESULT 2
LOCUS AB016072 2816 bp mRNA PRI 06-FEB-1999
DEFINITION Homo sapiens mRNA for p51A, complete cds.
ACCESSION AB016072
VERSION AB016072.1 GI:3510327
KEYWORDS p51A.
SOURCE Homo sapiens skeletal muscle cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Ikawa,S. and Osada,M.
TITLE Submitted (10-JUL-1998) to the DDBJ/EMBL/Genbank databases.
JOURNAL Shuntaro Ikawa, Institute of Development, Aging and Cancer,
Department of Cell Biology; 4-1 Seiry-machi, Sendai, Miyagi
Tel.81-22-717-8484, Fax.81-22-717-8488)
2 (sites)
REFERENCE
AUTHORS Osada,M., Ohba,M., Kawahara,C., Ishioke,C., Kanamaru,R., Katoh,I.,
Ikawa,Y., Nimura,Y., Nakagawara,A., Obinata,M. and Ikawa,S.
TITLE Cloning and functional analysis of human p51A, which structurally
and functionally resembles p53
JOURNAL Nat. Med. 4 (7), 839-843 (1998)
MEDLINE 98324755
FEATURES
source Location/Qualifiers
1..2816
/organism="Homo sapiens"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 61 gatttctggaacagcctatatgttcagttcagccattgacttgaacttgtgatgaa 120
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Db 205 GATTTCTGGAAACCGCTATATGTTCACTTCAGCCCTTGAACCTTGTGTGATGAA 264
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Db 445 CAGAACAGCGTCACGGGCGCCTTCCCTTACGACACGCCAGCTCACCCTTGATGCTCTC 504
Oy 361 tctccatcaaccgcatccctcccaacacagcactacccaagcccgccagtttcagagtg 420
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Oy 421 tccctcagcagctgagcaaccgcaagtcggcaacctgagacgtattccactgaactgaag 480
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Db 565 TCTTCTCCAGCAGTGCAGCACACCGCCACGCTGAGAGTTCCTACAGAACTGAG 624
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Oy 601 gtgttgaaagcgtgcccacaacatgagctgagccgtgaattcaacgagggagacattggc 660
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Db 745 GTGTGAAAGCGTCCCAACCATGAGCTGAGCGGTGAATTCACAGGAGCAATTTGCC 804
Oy 661 cctcctagtcattgattcagtagagaggagagacatgcccagttatgtgaagatccc 720
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Db 805 CCTCTGTATCTTTGATTTCAGTGAAGGAGACAGCCATGCCCATGTATGTAAGATATCC 864
Oy 721 atcacagaagacagagtgctgtgtactatgagccaacccaggttggcactgaatc 780
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QY	841	ccaatttaatactcttactctctgtgaaacccgaatctggccaagtccctggccgcagctgc	900
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Db	1285	TCCCTGGAACTCATGACAGTACTTCTCTCAGCACACAAATTTGAAGCTNAAGCAACAGCA	1344
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VERSION	AF075432				
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ORGANISM	human.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 1551)				
AUTHORS	Yang,A., Kaghad,M., Wang,Y., Gillett,E., Fleming,M.D., Dotsch,V.,				
TITLE	Andrews,N.C., Caput,D. and McKeon,F.				
JOURNAL	p53, a p53 homolog at 3q27-29, encodes multiple products with				
REFERENCE	transactivating, death-inducing, and dominant-negative activities				
AUTHORS	MO1. Cell 2 (3), 305-316 (1998)				
JOURNAL	98448095				
MEDLINE	2 (bases 1 to 1551)				
REFERENCE	Yang,A., Kaghad,M., Caput,D. and McKeon,F.				
AUTHORS	Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240				
TITLE	Longwood Ave, Boston, MA 02115, USA				
JOURNAL	Location/Qualifiers				
FEATURES	1..1551				
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QY	661	ccccctcagtcattgtatccgtagtagaggggaacgcataigcccaatgatactagaatccc	72
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RESULT	4			
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LOCUS	AF075430	1926 bp	mRNA	PRI
DEFINITION	Homo sapiens TA p53 alpha mRNA, complete cds.			04-OCT-1998
ACCESSION	AF075430			
VERSION	AF075430.1	GI:3695081		
KEYWORDS	.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1926)			
AUTHORS	Yang,A., Kaghad,M., Wang,Y., Gillette,E., Fleming,M.D., Dotsch,Y., Andrews,N.C., Caput,D. and McKee,F. p63, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities Mol. Cell 2 (3), 305-316 (1998)			
TITLE				
JOURNAL				
MEDLINE	98448095			
REFERENCE	2 (bases 1 to 1926)			
AUTHORS	Yang,A., Kaghad,M., Caput,D. and McKee,F. Direct Submision			
TITLE	Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240 Longwood Ave, Boston, MA 02115, USA			
JOURNAL				
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AUTHORS	1 (bases 1 to 2270)		
TITLE	Ikawa,S. and Osada,M.		
JOURNAL	Submitted (10-JUL-1998) to the DDBJ/EMBL/GenBank databases. Shuntaro Ikawa, Institute of Development, Aging and Cancer, Department of Cell Biology; 4-1 Setryo-machi, Sendai, Miyagi 980-8575, Japan (E-mail:sikawa@idac.tohoku.ac.jp, Tel:81-22-717-8484, Fax:81-22-717-8488)		
REFERENCE	2 (sites)		
AUTHORS	Osada,M., Ohba,M., Kawahara,C., Ishioka,C., Kanamaru,R., Katoh,I., Ikawa,Y., Minura,Y., Nakagawara,A., Ohinata,M. and Ikawa,S.		
TITLE	Cloning and functional analysis of human p51, which structurally and functionally resembles p53		
JOURNAL	Nat. Med. 4 (7), 839-843 (1998)		
MEDLINE	98324755		
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 ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 4846)
 Bamberger, C., Paul, D., Augustin, M. and Schmale, H.
 Tumour suppressor genes of the p53 family
 Patent: WO 9961610-A 2 02-DEC-1999;
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 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 4849)
 AUTHORS Schmale, H.
 TITLE Direct Submission
 JOURNAL Submitted (24-MAR-1998) H. Schmale, Institut f. Zellbiochemie und,
 Klinische Neurobiologie, Universitätskrankenhaus Eppendorf,

REFERENCE 2 (bases 1 to 4849)
 AUTHORS Augustin, M., Bamberg, C., Paul, D. and Schmale, H.
 TITLE Cloning and chromosomal mapping of the human p53-related KET gene to chromosome 3q27 and its murine homolog Ket to mouse chromosome 16
 JOURNAL Mamm. Genome 9 (11), 899-902 (1998)
 MEDLINE 99018225
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 Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtccagagcacacagacaagaatgaattccctcagtcagagagtttccagacatcttg 60
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 DB 145 ATGTCCAGAGCACACAGACAAGAAATGCTCTCAGTCAGAGGTTTCCAGCATATCTGG 204
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 QY 61 gattcttgaaagcctatatgtttagttcagcccatgaacttgaaactttgttgatgaa 120
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 DB 205 GATTTCGTGGAACAGCCTATATGTTCAGTTCAGCCCATGTGAACTTGTGTGATGAA 264
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 ccatcagaagaatggttcgacaacaagaatgagaatgaatgagatgagatglatccgacatg 180
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 DB 265 CCATCAGAGAAGTGTGCGACAAACAAGATTGAGATTAGCATGAGCATGTATCCGATCGAG 324
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 QY 181 gactcggaactgagtgagccccaatggtgcacagatgacgaacactggtggctctgaaacagc 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 325 GACTCGGAGACTGAGTGAACCCCATGTGGCCACAGTACGAACCTGGGGCTCTCTGAACAGC 384
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 QY 241 atggaacagagatgtaagaacggtctctgtccacagagtcctccttaacagacagacagcg 300
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 QY 301 cagaacagcgttcacagcgccctcgccctacgacagcccaagctcacacttcgatgctctc 360
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 DB 445 CAGAAGACGCGTCAAGGGGCGCTCGCCCTACGACAGCCCACTCCTTGATGAGTCTCTC 504
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 QY 361 tctcacaacccgcatcctcctcacaacagactaccagagcccgacagatgctgacgtg 420
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 QY 421 tctctcagaagctgagacacgccaagtcggccactcggaagctattcactgaactgaag 480
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DB 565 TCCTCCAGCAGTGTGACACCGCCCAAGTCCGCCACTCGAGCTTTTCCACTGAGACTAAG 624
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 DB 805 CCTCTAGTCAATTGATTCGAGTGAAGGGGAACCCATGCGCCAGTATGTGAAAGATCCC 864
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 QY 721 atcaagaagaacagagatgtgtgtgtatcctatgagccaccccggttggacatgattc 780
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 DB 865 ATCAGAGAAAGACAGAGTGTGCTGTACCTTATGAGCCACCCAGGTGGCATGAAATTC 924
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 QY 781 acgacagctctgtacaaattcatgtagtaacagcagttgtgttgaggagatgaaccgct 840
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 DB 1045 TTTAGGCCCGCGATCTGTCTGTGCCAGGAAGACAGAGGAGGCGGATGAAGATAGCATC 1104
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 DB 1105 AGAAGACAGCAAGTTGTGAGACATGACAAAGACGATGATGTAGAAAGCCGCTTTGCT 1164
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 QY 1201 cagcagcagcagcagcacttacttcagaagaaca 1232
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RESULT 9
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 LOCUS AF075429
 DEFINITION Homo sapiens DN p53 gamma mRNA, complete cds.
 ACCESSION AF075429
 VERSION AF075429.1 GI:3695079
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1182)
 AUTHORS Yang, A., Kagnad, M., Wang, Y., Gillett, E., Fleming, M.D., Dotsch, V.,
 Andrews, N.C., Caput, D. and McKeon, F.
 TITLE p53, a p53 homolog at 3q27-29, encodes multiple products with
 transactivating, death-inducing, and dominant-negative activities
 JOURNAL Mol. Cell 2 (3), 305-316 (1998)

MEDLINE 98448095
 REFERENCE 2 (bases 1 to 1182)
 AUTHORS Yang, A., Kaghad, M., Caput, D. and McKeon, F.
 TITLE Direct Submission
 JOURNAL Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240
 Longwood Ave, Boston, MA 02115, USA
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 /chromosome="3"
 /map="3q27-q29"
 1. 1182
 /function="transcription factor"
 /note="second splice variant; related to p3 and p73"

CDS

/product="DN p53 gamma"
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 /db_xref="GI:3695080"
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 EGQIAPPSHLIRVGNHAQVIEDPIRGROSVLPPEPVGEFTVLVNFMCNSSC
 VGGNRRPILITLITLRTDQVIGRRCFEARICAPGRDRKADSDIRKQVSDSTKN
 CDGKRPFRONTHTIOMSTIKKRSPPDELLYLPVRGRREYEMILIKESLEIMQYLP
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BASE COUNT 330 a 342 c 276 g 234 t
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Query Match

Best Local Similarity 84.9%; Score 1140.6; DB 88; Length 1182;
 Matches 1152; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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 Db 9 CCTGAAACAAATGCCCACTCAATTAGTGAACCACTACAGAACTGGGGCTCTCT 68
 Oy 234 gaacagatggacagcagatcgaagatcgaagcgtcctcgtccacagctccctatacaga 233
 Db 69 GAACAGATGACCCAGACGATTCAGAACGGGCTCCTCGTCACACAGTCCCATACACAGA 128
 Oy 294 ccaacgcagagaacagcgtcagcagcgcctcgcctccatcagcagccacagctccactcga 353
 Db 129 CCACGGCAGAAAGCCTACACGGCCGCTCGCTACGACACACGCTCCACCTTCCA 188
 Oy 354 tgcctctctccatccacccgcatccctccacacacagctacccagcgcgcagatgtt 413
 Db 189 TGCCTCTCTCCATCAACCCGCCCTCCCTCAACACGCACTACCCAGGCCCGACAGCTT 248
 Oy 414 cgaacgtgctccagcagatcgaagcagcgcacagctgagcagctggagctatccactga 473
 Db 249 CGAGGTGCTCTTCACAGATCGACGACCGCAAGTGGCCACTGACATTCACACTGA 308
 Oy 474 acggaagaactctactgcacaattgcaagaacatgccacatccagatcaagtgatgac 533
 Db 309 ACTGAAGAAACTCTACTGCCAAATTCGAAGAATGCCCAATCCAGATCAAGGTATGAC 368
 Oy 534 ccaacgtcctcagagagcgtgtatccgcgcagctgctgtctacaaaaaagctgagcagct 593
 Db 369 CCCACTCTCTCAGGAGCGTGTATCCGCCCATGCTGTCTCAAAAAAAGCTGAGACACGT 428
 Oy 594 caccgaggtggtgtagagcgtgtcccaacatgagctgagccgttgatccaagaggagca 653
 Db 429 CACGGAGTGTGTGAAGCGGTGCCCAACATGAGCTGAGCCGTGAATTCACAGAGGAGCA 488
 Oy 654 gattgcctcctctagtcatttgatccgtagagggaggaacagcagctccagatgtaga 713
 Db 489 GATTCGCCCTCTACTGATTTGATTCGAGTAGAGGGAACAGCCATGCCAGTATGTAGA 548
 Oy 714 aatcccatcaaggaagcagagtgctgctactatagccacccagctggagac 773

Db 549 AGATCCCATCAGACAGACAGAGTGTCTGTGATACCTTATGACCAACCCAGGTGGCAC 608
 Oy 774 tgaattcagacagctctgtacaatttcatalgtgtaacagcagctgtgtggaagatga 833
 Db 609 TGAATTCACGACACTCTTGTATCAATTTCAATTCATGTGTAAACAGAGTGTGTGAGGATGA 668
 Oy 834 ccgcgcctcaatttaattcatcttactctggaacacagagatgggcaagctcctggcgcg 893
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 Oy 894 acgctgcttgagggcccgagctcgtgcttgccaggaagaagacaggaagcgatgaga 953
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 Oy 1254 gaatgacctgtgagcccccagagagaaccccaaaactctacgctctctcttaaga 1313
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 Oy 1314 ttccaagcccccaacagcagatcagttaccga 1344
 Db 1149 TTCCAAGCCCCCAACCATGATCAGTACCA 1179

RESULT 10
 AF075434
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 1 (bases 1 to 1452)
 Yang, A., Kaghad, M., Wang, Y., Gillette, E., Fleming, M.D., Dotsch, V.,
 Andrews, N.C., Caput, D. and McKeon, F.
 p53, a p53 homolog at 3q27-29, encodes multiple products with
 transactivating, death-inducing, and dominant-negative activities

1. 1452
 2 (bases 1 to 1452)
 Yang, A., Kaghad, M., Caput, D. and McKeon, F.
 Direct Submission
 Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240
 Longwood Ave, Boston, MA 02115, USA

FEATURES

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 /organism="Mus musculus"
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 1. 1452
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CDS

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/db_xref="GI:3695090"
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PSPALPSTNDIPGHSFDVFSQSSSTASATVSTELKLTQIAKTPDQIKWTP
PDQGVIRAMAPYKRAEHVEYKRPNHIELSRENEQIAPSHLIRVEGSHAOY
EDPITGROSVLPYEPVGTEFTVLVNFMCNCSGVGMNRPLIITLETROGV
LGRCFEARIACPGDRKADDSIRKQVSDSANGDAFNRQNGIOWTSKRRSP
DDELYLPYRGREYEMLIKIKESLEIMQYLPQHTLEMYRQOQOQHLLKHLISA
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BASE COUNT      394 a      427 c      341 g      290 t
ORIGIN

Query Match      83.4%; Score 1121.2; DB 94; Length 1452;
Best Local Similarity 90.3%; Pred. No. 2.4e-284;
Matches 1214; Conservative 0; Mismatches 118; Indels 12; Gaps 1;

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DB 118 ATGTCCAGAGCACACGACCAAGAGAGTTCCTCAGCCAGAGTCTCCAGCATCTG 177
QY 61 gatttcggaacagcctatagtctcagtcagccattgaaacttctgtgaa 120
DB 178 GATTTCGTGGAACAGCCTTATCTCAGTACAGCCCATGAGTTGAACTTTGGATGAA 237
QY 121 catatgaagatgtgtcgcaaaagaattgattgatagtacgtgtatccgacgag 180
DB 238 CCTCCGAAATAGTGTCACAAACAAAGATTGAGATTGAGATTGATCCCATGCAA 297
QY 181 gactcgagactgagtcagcccatgtgtccacagtcagaaactcggtcctcgaaacagc 240
DB 298 GACTCGAGACTGAGTCAGCCCATGTGCGCACAGTACAGAACTGGGGGCTCCGAAACGC 357
QY 241 atggacagcagatctagaagagcgtcctcgtccacagtcctcatatacacagacagcg 300
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QY 301 cagaagacgtcacagcgccctcgcctcgcacagcccaagtcacacgttcagatgctctc 360
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QY 361 tctccatcacccgcctacccctcccaacacagactaacccagcccgacagtttcgacgtg 420
DB 478 TCTCCATTCCTCCCTTCCTCCACAGATTTACCCGGCCACACAGCTTCGATGTG 537
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QY 661 cctccagatcattgtgtgagatagaggaggaagacacatgcccagatgtagaagatccc 720
DB 778 CCTCCAGATATGTGATGAGTAGAAGGAAAGCAGCATGCCAGATGTGAGAAATCTCT 837
QY 721 atcacagagacagagtgctgtgactctatgagcaccacccaggttggcactgaattc 780
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QY 781 agcagcgtctgtacaaattcatatgtgttaacagcagtggtgtgagggatgaaccgcgt 840
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QY 841 ccaatttatactcttactctggaacacagagatggggaagctcctgggccaagctgc 900
DB 958 CCAATTTTAACTCTGTTACTCTGGAACACAGATGGCAATCTCTGGGCCACAGCTGC 1017
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QY 1201 cagcagcagcagcagcagcacttaccagaaacatctccttcagcccgcttcagaaatgag 1260
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QY 1261 ctgttgagcccgagagagaactcccaaaactctgaagctctctttagacattccaa 1320
DB 1366 CTGTGTGAGGCCCGGGGAGAGAGCTCCGACACAGTGTGACGCTTCTTATGACATTCAC 1425
QY 1321 ccccccaacccgacatgtagtccca 1344
DB 1426 CCCCCAAACCATCTCGGTATCCCA 1449

RESULT 11
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LOCUS AF075435
DEFINITION Mus musculus TA*p53 beta mRNA, complete cds.
ACCESSION AF075435
VERSION AF075435.1 GI:3695091
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1668)
AUTHORS Yang, A., Kaghad, M., Wang, Y., Gilliet, E., Fleming, M. D., Dotsch, V.,
Andrews, N. C., Caput, D. and McKeon, F.
p53, a p53 homolog at 3q27-29, encodes multiple products with
transactivating, death-inducing, and dominant-negative activities
Mol. Cell 2 (3), 305-316 (1998)
JOURNAL 98448095
MEDLINE
REFERENCE 2 (bases 1 to 1668)
AUTHORS Yang, A., Kaghad, M., Caput, D. and McKeon, F.
Direct Submission
Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240
Longwood Ave, Boston, MA 02115, USA
FEATURES
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/Note="second splice variant; related to p53 and p73"
CDS

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380 g
325 t

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Query Match	78.7%;	Score 1057.6;	DB 94;	Length 1668;
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LOCUS	AF075436	2043 bp	mRNA
DEFINITION	Mus musculus	TA*P63 alpha mRNA,	complete cds.
ACCESSION	AF075436		
VERSION	AF075436.1	GI:3695093	

ORGANISM	REFERENCE
House mouse:	
Mus musculus	1 (bases 1 to 2043)
Eukaryota; Metazoa:	
Chordata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia;	
Sclurognathi; Muridae; Murinae; Mus	

AUTHORS	Yang, A., Kagniad, M., Wang, Y., Gilllett, E., Fleming, M.D., Dotsch, V., Andrews, N.C., Caput, D., and Mckoon, P.
TITLE	p53, a p53 homolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities
JOURNAL	Mol. Cell. 2 (3), 305-316 (1998)
PMID	9841900
MEDLINE	

AUTHORS Yang, A., Kaqhad, M., Caput, D. and McKeon, F.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-1998) Cell Biology, Harvard Medical School, 240 Longwood Ave. Boston, MA 02115, USA

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DEFINITION Homo sapiens p53 homolog (p40) mRNA, complete cds.
ACCESSION AF061512
VERSION AF061512.1 GI:3273744
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2082)
AUTHORS Trink, B., Wu, L., Okami, K., Siurupong, V., Jen, J. and Sidransky, D.
TITLE Direct Submission
JOURNAL Submitted (24-APR-1998) Otolaryngology-Head & Neck Surgery, The
Johns Hopkins School of Medicine, 720 Rutland Ave., Baltimore, MD
21205-2196, USA

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Claim 3; Page 148-151; 163pp; Japanese.
PS
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CC activity. The p51 gene can be used in the investigation, diagnosis and
CC treatment of diseases such as cancer, with which the p53 family cell
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Conservatively	100.0%	Pred. No. 0;	
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ID AAC66029	standard. 2001. 2011. 2012. 2013. 2014. 2015. 2016. 2017. 2018. 2019. 2020. 2021. 2022. 2023. 2024. 2025. 2026. 2027. 2028. 2029. 2030. 2031. 2032. 2033. 2034. 2035. 2036. 2037. 2038. 2039. 2040. 2041. 2042. 2043. 2044. 2045. 2046. 2047. 2048. 2049. 2050. 2051. 2052. 2053. 2054. 2055. 2056. 2057. 2058. 2059. 2060. 2061. 2062. 2063. 2064. 2065. 2066. 2067. 2068. 2069. 2070. 2071. 2072. 2073. 2074. 2075. 2076. 2077. 2078. 2079. 2080. 2081. 2082. 2083. 2084. 2085. 2086. 2087. 2088. 2089. 2090. 2091. 2092. 2093. 2094. 2095. 2096. 2097. 2098. 2099. 2100. 2101. 2102. 2103. 2104. 2105. 2106. 2107. 2108. 2109. 2110. 2111. 2112. 2113. 2114. 2115. 2116. 2117. 2118. 2119. 2120. 2121. 2122. 2123. 2124. 2125. 2126. 2127. 2128. 2129. 2130. 2131. 2132. 2133. 2134. 2135. 2136. 2137. 2138. 2139. 2140. 2141. 2142. 2143. 2144. 2145. 2146. 2147. 2148. 2149. 2150. 2151. 2152. 2153. 2154. 2155. 2156. 2157. 2158. 2159. 2160. 2161. 2162. 2163. 2164. 2165. 2166. 2167. 2168. 2169. 2170. 2171. 2172. 2173. 2174. 2175. 2176. 2177. 2178. 2179. 2180. 2181. 2182. 2183. 2184. 2185. 2186. 2187. 2188. 2189. 2190. 2191. 2192. 2193. 2194. 2195. 2196. 2197. 2198. 2199. 2200. 2201. 2202. 2203. 2204. 2205. 2206. 2207. 2208. 2209. 2210. 2211. 2212. 2213. 2214. 2215. 2216. 2217. 2218. 2219. 2220. 2221. 2222. 2223. 2224. 2225. 2226. 2227. 2228. 2229. 2230. 2231. 2232. 2233. 2234. 2235. 2236. 2237. 2238. 2239. 2240. 2241. 2242. 2243. 2244. 2245. 2246. 2247. 2248. 2249. 2250. 2251. 2252. 2253. 2254. 2255. 2256. 2257. 2258. 2259. 2260. 2261. 2262. 2263. 2264. 2265. 2266. 2267. 2268. 2269. 2270. 2271. 2272. 2273. 2274. 2275. 2276. 2277. 2278. 2279. 2280. 2281. 2282. 2283. 2284. 2285. 2286. 2287. 2288. 2289. 2290. 2291. 2292. 2293. 2294. 2295. 2296. 2297. 2298. 2299. 2300. 2301. 2302. 2303. 2304. 2305. 2306. 2307. 2308. 2309. 2310. 2311. 2312. 2313. 2314. 2315. 2316. 2317. 2318. 2319. 2320. 2321. 2322. 2323. 2324. 2325. 2326. 2327. 2328. 2329. 2330. 2331. 2332. 2333. 2334. 2335. 2336. 2337. 2338. 2339. 2340. 2341. 2342. 2343. 2344. 2345. 2346. 2347. 2348. 2349. 2350. 2351. 2352. 2353. 2354. 2355. 2356. 2357. 2358. 2359. 2360. 2361. 2362. 2363. 2364. 2365. 2366. 2367. 2368. 2369. 2370. 2371. 2372. 2373. 2374. 2375. 2376. 2377. 2378. 2379. 2380. 2381. 2382. 2383. 2384. 2385. 2386. 2387. 2388. 2389. 2390. 2391. 2392. 2393. 2394. 2395. 2396. 2397. 2398. 2399. 2400. 2401. 2402. 2403. 2404. 2405. 2406. 2407. 2408. 2409. 2410. 2411. 2412. 2413. 2414. 2415. 2416. 2417. 2418. 2419. 2420. 2421. 2422. 2423. 2424. 2425. 2426. 2427. 2428. 2429. 2430. 2431. 2432. 2433. 2434. 2435. 2436. 2437. 2438. 2439. 2440. 2441. 2442. 2443. 2444. 2445. 2446. 2447. 2448. 2449. 2450. 2451. 2452. 2453. 2454. 2455. 2456. 2457. 2458. 2459. 2460. 2461. 2462. 2463. 2464. 2465. 2466. 2467. 2468. 2469. 2470. 2471. 2472. 2473. 2474. 2475. 2476. 2477. 2478. 2479. 2480. 2481. 2482. 2483. 2484. 2485. 2486. 2487. 2488. 2489. 2490. 2491. 2492. 2493. 2494. 2495. 2496. 2497. 2498. 2499. 2500. 2501. 2502. 2503. 2504. 2505. 2506. 2507. 2508. 2509. 2510. 2511. 2512. 2513. 2514. 2515. 2516. 2517. 2518. 2519. 2520. 2521. 2522. 2523. 2524. 2525. 2526. 2527. 2528. 2529. 2530. 2531. 2532. 2533. 2534. 2535. 2536. 2537. 2538. 2539. 2540. 2541. 2542. 2543. 2544. 2545. 2546. 2547. 2548. 2549. 2550. 2551. 2552. 2553. 2554. 2555. 2556. 2557. 2558. 2559. 2560. 2561. 2562. 2563. 2564. 2565. 2566. 2567. 2568. 2569. 2570. 2571. 2572. 2573. 2574. 2575. 2576. 2577. 2578. 2579. 2580. 2581. 2582. 2583. 2584. 2585. 2586. 2587. 2588. 2589. 2590. 2591. 2592. 2593. 2594. 2595. 2596. 2597. 2598. 2599. 2600. 2601. 2602. 2603. 2604. 2605. 2606. 2607. 2608. 2609. 2610. 2611. 2612. 2613. 2614. 2615. 2616. 2617. 2618. 2619. 2620. 2621. 2622. 2623. 2624. 2625. 2626. 2627. 2628. 2629. 2630. 2631. 2632. 2633. 2634. 2635. 2636. 2637. 2638. 2639. 2640. 2641. 2642. 2643. 2644. 2645. 2646. 2647. 2648. 2649. 2650. 2651. 2652. 2653. 2654. 2655. 2656. 2657. 2658. 2659. 2660. 2661. 2662. 2663. 2664. 2665. 2666. 2667. 2668. 2669. 2670. 2671. 2672. 2673. 2674. 2675. 2676. 2677. 2678. 2679. 2680. 2681. 2682. 268

AAC66029;

Human lung cancer-associated cDNA p63 isoform 3.
21-FEB-2001 (first entry)

KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 KW vaccine; detection; ss.
 XX
 XX

homo sapiens.
WO200061612-A2.

PD 19-OCT-2000.
XX
03-APR-2000; 2000MO-US08896.
X

02-APR-1999; 99US-0285479.
17-DEC-1999; 99US-0466396.
30-DEC-1999; 99US-0476496.

A
 {CORI-) CORTYA COMP
 R 10-JAN-2000; 2000US-0480884.
 R 22-FEB-2000; 2000US-0510376.
 X

PI Wang T, Fan L;
XX MPI; 2000-628399/60.
DR P-PSDB; AAB11359.
XX
XX Isolated polypeptide comprising an immunogenic portion of a lung tumor
PT protein is used for detecting and monitoring progression of lung cancer
PT in a patient -
XX
XX Claim 25a; Page 238-239; 261pp; English.
PS
XX
XX This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit
CC development of cancer.
CC
XX
SQ Sequence 2816 BP; 781 A; 658 C; 619 G; 758 T; 0 other;

Query Match 100.0%; Score 1344; DB 21; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtccagagcagacagacaataatgtctcagtcacagagttttccagcatcttg 60
Db 145 atgtccagagcagacagacaataatgtctcagtcacagagttttccagcatcttg 204
QY 61 gatcttctgaaagcagctatatgttcagttcagcccatctactgtgaactttgtgatga 120
Db 205 gatcttctgaaagcagctatatgttcagttcagcccatctactgtgaactttgtgatga 264
QY 121 ccatcagaagaatgtgtcgacaaacaagaattgagattagacatgtgactgtatccgcatgca 180
Db 265 ccatcagaagaatgtgtcgacaaacaagaattgagattagacatgtgactgtatccgcatgca 324
QY 181 gactcgaagcttgatgacccatgttgccacagtaacagacacttggtggccctcgaaagac 240
Db 325 gactcgaagcttgatgacccatgttgccacagtaacagacacttggtggccctcgaaagac 384
QY 241 atgagacagcagattcagaacggctcctctgtccacagtcctctataacacagacacgag 300
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QY 301 cagaacagcgtcagcgcgccctgcctcagcagacgacccagctccaccttgatgtcttc 360
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Db 805 cctccagtcatttgattgattgagtagagggaaacagacatgcccagatagtagaagatccc 864
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Db 1225 ctgttatacttaccagtgagggccggtgagacttatgaaatgctgtgaaatcaaaag 1284
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QY 1261 ctgtgtgagcccggaagagaacatccaaacatctgaacttctctttagacattccaa 1320
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QY 1321 cccccaacccgatacgtgtaccca 1344
Db 1465 cccccaacccgatacgtgtaccca 1488

RESULT 3
AAK58574
ID AAK58574 standard; cDNA; 1347 BP.
XX
XX AAK58574;
AC
XX 16-AUG-1999 (first entry)
DT
XX
DE Human cell regulatory protein p63, isoform huTap63 gamma, cDNA.
XX
XX Cell regulatory protein; p63; huTap63 gamma; Tap63 gamma; human;
KW cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy; ss.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_difference 1254
FT
FT /*tag= a
FT /note= "this base represents a nucleotide missing
FT from the sequence given in the
FT specification. It is included to maintain
FT the nucleotide numbering given in the

Specification for this sequence*

FT
 XX
 PN M09919357-A2.
 XX
 PD 22-APR-1999.
 XX
 PE 02-OCT-1998; 98MO-US21992.
 XX
 PR 29-MAY-1998; 98US-0087216.
 PR 15-OCT-1997; 97US-0062076.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI McKeon F., Yang A.
 XX
 DR WPI: 1999-277595/23.
 DR P-SDB: AAY05955.
 XX
 PT New isolated p63 cell regulatory protein for, e.g. treatment of
 PT tumours
 XX
 PS Claim 1; Fig 11; 161pp; English.
 XX
 CC The present invention concerns the discovery of a new family of
 CC cell regulatory proteins (CRPs) termed the p63 family of proteins,
 CC which demonstrate certain sequence identity to known tumour
 CC suppressor proteins p53 and p73. It has been observed that the
 CC intron-exon organisation is conserved between p73 and p53, and from
 CC known exon and intron sizes for these 2 genes, it was possible to
 CC of amplifying new members of this gene family using a PCR-based strategy
 CC Inttron. The human p53 gene was localised to chromosomal position
 CC 3q27-29. At least 6 different isoforms exist. Splice variants
 CC differing at the C-terminus have been designated as alpha, beta and
 CC gamma forms, while p63 members have been designated as alpha, beta and
 CC designated as delta and TA forms, where the delta form lacks the
 CC transactivation domain. The present sequence represents a cDNA
 CC clone encoding human TA-p63 gamma. p63 was detected in a variety of
 CC human and mouse tissue. It demonstrates remarkably divergent
 CC activities, such as the ability to transactivate p53 reporter genes
 CC and induce apoptosis. Cessation or down regulation of p63 expression
 CC may play a critical role in the process of cervical squamous
 CC differentiation, both benign and neoplastic. Delta isoforms of p63
 CC act as dominant negatives towards transactivation by p53 and p63.
 CC p63 may also be implicated in hematopoiesis, muscle wasting (e.g.
 CC cachexia) and neuronal differentiation and related degenerative
 CC disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see
 CC AAY58572-83) and anti-p63 antibodies of the invention can be used to
 CC identify compounds useful for treating disorders involving such
 CC processes, in detection and diagnosis, and in the production of
 CC transgenic animals.
 XX
 SQ Sequence 1347 BP; 374 A; 381 C; 316 G; 275 T; 1 other;

Query Match 99.9%; Score 1343; DB 20; Length 1347;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1343; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atgtcccaagacacacagaacaatgaattcctcagtcacagagtttccacatattg 60
 Db 1 atgtcccaagacacacagaacaatgaattcctcagtcacagagtttccacatattg 60
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 Db 121 ccataagaagatgtgtgacacaagaattgagattgagatgagactatccgacag 180
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 Db 421 tctcttcagcagatcgacacgcgcgaagtgcgcacctgagcgtatccatcgaaatg 480
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 Db 721 atcaagaagaacagagtggtgtgtgtacattatgagcaccacaggttcgacatgattc 780
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 Db 781 agcagagctctgtacaaatttcattatgtgtaacagcagtggtgtgagggatgagccg 840
 QY 841 ccaatttaactattgttactctggaacacagagatggcgaagtcctgagccagctgc 900
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 Db 1141 tcccttgagaaactatgacgttccctccacagaacatgaaagctgacagcagcaaa 1200
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QY 1321 ccccaaacgcatggtaccca 1344
 Db 1321 ccccaaacgcatggtaccca 1344

RESULT 4

AAVS8573
 ID AAVS8573 standard; cDNA; 1551 BP.

AAVS8573;

16-NOV-1999 (first entry)

Human cell regulatory protein p63, isoform hUTAP63 beta, cDNA.

Cell regulatory protein; p63; hUTAP63 beta; TAP63 beta; human; cancer; tumour suppressor; cell cycle control; apoptosis; cell proliferation; cell differentiation; therapy; ss.

Homo sapiens.

MO9919357-A2.

22-APR-1999.

02-OCT-1998; 98MO-US21992.

29-MAY-1998; 98US-0087216.

15-OCT-1997; 97US-0062076.

(HARD) HARVARD COLLEGE.

McKeon F, Yang A;

WPI; 1999-277595/23.

P-PSDB; AAY05954.

New isolated p63 cell regulatory protein for, e.g. treatment of tumours

Claim 1; Fig 10; 161pp; English.

The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins,

which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the

intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes, it was possible to

identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening

intron. The human p53 gene was localised to chromosomal position 3q27-29. At least 6 different isoforms exist. Splice variants

differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members differing in the N-terminus are

designated as delta and TA forms, where the delta form lacks the transactivation domain. The present sequence represents a cDNA

clone encoding human TAP63 beta. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent

activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p63 expression

may play a critical role in the process of cervical squamous differentiation, both benign and neoplastic. Delta isoforms of p63

act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative

disorders. p63 polypeptides (see AAY05953-64), polynucleotides (see AAY5572-83) and anti-p63 antibodies of the invention can be used to

identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of

transgenic animals.

Sequence 1551 BP; 425 A; 466 C; 350 G; 310 T; 0 other;

Query Match 91.7%; Score 1232; DB 20; Length 1551;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtccagagcagacagacaaatgaatttcctcagtcagaggtttccagcatatcg 60
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 QY 421 tctctcagcagtcagacagccagcgaagtcgacacactgagcgtatccactgagcgaag 480
 Db 421 tctctcagcagtcagacagccagcgaagtcgacacactgagcgtatccactgagcgaag 480
 QY 481 aaactctactgcgaatattgcaagaacatgcccatacagaatgtagtaccacact 540
 Db 481 aaactctactgcgaatattgcaagaacatgcccatacagaatgtagtaccacact 540
 QY 541 cctcagagagcgtttatccgcgcacatgctgtctataaaaaaactgagacagcgag 600
 Db 541 cctcagagagcgtttatccgcgcacatgctgtctataaaaaaactgagacagcgag 600
 QY 601 gtgtgagagcggtgcccacacatgagctgagcgttgatattcaacagagagcagattgac 660
 Db 601 gtgtgagagcggtgcccacacatgagctgagcgttgatattcaacagagagcagattgac 660
 QY 661 cctcctagcatttgatcagtagagaggggaacagccatgcccagattgtagaagatccc 720
 Db 661 cctcctagcatttgatcagtagagaggggaacagccatgcccagattgtagaagatccc 720
 QY 721 atcacaggaagacagagtggtggtgtacctaagagccacccaggttgacatgaattc 780
 Db 721 atcacaggaagacagagtggtggtgtacctaagagccacccaggttgacatgaattc 780
 QY 781 acgacagctgtgacaaattcatggtgaacagcagtggtgtgagagatgaaacccggt 840
 Db 781 acgacagctgtgacaaattcatggtgaacagcagtggtgtgagagatgaaacccggt 840
 QY 841 ccaatttaactctgttactctggaacacagagatggaagtcctgagcagcgtgc 900
 Db 841 ccaatttaactctgttactctggaacacagagatggaagtcctgagcagcgtgc 900
 QY 901 ttgtgagccgagtggtgtgttccagagagagagagagcagagcgatgaaataagatc 960
 Db 901 ttgtgagccgagtggtgtgttccagagagagagagagcagagcgatgaaataagatc 960
 QY 961 agaaagcagcaagtttcgagcagatacaagaacggtgatgtgacgaagcggcttgcgt 1020
 Db 961 agaaagcagcaagtttcgagcagatacaagaacggtgatgtgacgaagcggcttgcgt 1020

Db 841 ccaattttatcatattgtttacccttcggaacaacagagatctggaacgttcctggccgacgtc 900

Qy 901 ttgtgagcccgagatctgtgtcttgcgcggaagaagacaggaagcggaataagaatgac 960

Db 901 ttgtgagcccgagatctgtgtcttgcgcggaagaagacaggaagcggaataagaatgac 960

Qy 961 aaaaagcgcagacttctggagacagatacaaaagacgtgtgatacgtaagcccggttcgt 1020

Db 961 agaaaagcgcagacttctggagacagatacaaaagacgtgtgatacgtaagcccggttcgt 1020

Qy 1021 cagaacacacatctgtatccagatgataccatcaagaacagagatcccccagatgataa 1080

Db 1021 cagaacacacatctgtatccagatgataccatcaagaacagagatcccccagatgataa 1080

Qy 1081 ctgtatatcttaccagatggaaggcgcttgagacttatagaaatgcttctgaagatcaaaag 1140

Db 1081 ctgtatatcttaccagatggaaggcgcttgagacttatagaaatgcttctgaagatcaaaag 1140

Qy 1141 tcccttgaaactcatctgcagtaacctctccagacacaaatgaaacgttaaggcaacagaa 1200

Db 1141 tcccttgaaactcatctgcagtaacctctccagacacaaatgaaacgttaaggcaacagaa 1200

Qy 1201 cagcagacagacacagcacttaacttcggaaca 1232

Db 1201 cagcagacagacacagcacttaacttcggaaca 1232

RESULT	7
AA25771	
ID	AA25771 standard; cDNA; 2270 BP.
XX	

AC AA225771;

DT 07-JAN-2000 (first entry)
 YY

Human p51 encoding cDNA B.

KW tumour suppression; diagnosis; ss.

Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	145..2070
FT		/*tag- a

PN W09950412-A1.

PD 07-OCT-1999.
xy

PF 24-MAR-1999; 99WO-JP01512.

PR 27-MAR-1998; 98JP-0100467.
XY

PA (SAKA) OTSUKA PHARM CO LTD.
PA (IKAWA) IKAWA Y

Ikawa Y, Ikawa S, Ohinata M.

DR WPI; 1999-591318/50.

147643241.

New p53 related human gene p51, useful for diagnosis, investigation and treatment of cancers and tumors.

agents - potential cell proliferation

Example 1; Page 154-156; 163pp; Japanese.

The present sequence represents a human p51 gene, which is related to p53 and has cell proliferation regulation and tumour suppression activity. The p51 gene can be used in the investigation, diagnosis and treatment of diseases such as cancer, with which the p53 family cell

CC proliferation regulation is associated. The p51 protein may be used for
CC screening potential agonists and antagonists of its regulatory function,
CC for use as drugs,
CC
XX
SQ Sequence 2270 BP; 595 A; 677 C; 500 G; 498 T; 0 other;

Query Match	91.7%	Score 1232;	DB 20;	Length 2270;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1232;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	atgtccacagacacagacanaatlgatattccctcagtcacagaggtttccagacatactg	60
Db	145	atgtccacagacacacagacanaatlgatattccctcagtcacagaggtttccagacatactg	20
QY	61	gattctctggagaaagcgcctatagtttcaatttcagttccagcccatgtgaacttgtgatgaa	120
Db	205	gattctctggagaaagcgcctatagtttcaatttcagttccagcccatgtgaacttgtgatgaa	264
QY	121	ccatcagaagaatgtgtgagacaaacaagaatttgatatagatatgagactgtatcccgatcag	180
Db	265	ccatcagaagaatgtgtgagacaaacaagaatttgatatagatatgagactgtatcccgatcag	324
QY	181	gactcggagacctgtggtatcccccatgtgtgcccagatcacaggaaacctgtggtgtcctctgaacgc	240
Db	325	gactcggagacctgtggtatcccccatgtgtgcccagatcacaggaaacctgtggtgtcctctgaacgc	300
QY	241	atggacacagacagattctcagaacgcgtcctctgtccacacaaatccctctaaacacagacacgcg	300
Db	385	atggacacagacagattctcagaacgcgtcctctgtccacacaaatccctctaaacacagacacgcg	444
QY	301	cagaaacagcgtcaacggtgcgcctctgcctcactacgacacagccagctcacacttcgatgtcttc	360
Db	445	cagaaacagcgtcaacggtgcgcctctgcctcactacgacacagccagctcacacttcgatgtcttc	504
QY	361	tctccacacacccgcacatccctccccaacacgcgacataccacagccgcgacagtttcgaagctg	420
Db	505	tctccacacacccgcacatccctccccaacacgcgacataccacagccgcgacagtttcgaagctg	564
QY	421	tccttcacagcagtcagagacacgcgcacagtcgcgcacactgtgagacttatccattgaactcgaag	480
Db	565	tccttcacagcagtcagagacacgcgcacagtcgcgcacactgtgagacttatccattgaactcgaag	624
QY	481	aaactctatgcaccaattgtgcagaagaacatgcccccatccagatcaaggtgatgacccacact	540
Db	625	aaactctatgcaccaattgtgcagaagaacatgcccccatccagatcaaggtgatgacccacact	684
QY	541	cctccagagagctgtatataccgcgcacatgctctgtctcacaanaaagctgagacgttcacgcgag	600
Db	685	cctccagagagctgtatataccgcgcacatgctctgtctcacaanaaagctgagacgttcacgcgag	744
QY	601	gtgggtgaagcgggtcccccacaacatgaaactgaaagccgtgaaattcaacagaaggagacagattgc	660
Db	745	gtgggtgaagcgggtcccccacaacatgaaactgaaagccgtgaaattcaacagaaggagacagattgc	804
QY	661	cctcctatgatacttgatttcgagtagtagagggaaacagacatgccccagatattgaaabaatccc	720
Db	805	cctcctatgatacttgatttcgagtagtagagggaaacagacatgccccagatattgaaabaatccc	864
QY	721	atcacaggaagaacagagatgtgtgtgtgtaacctatagagcaaccccaagtttggacacttgaaatc	780
Db	865	atcacaggaagaacagagatgtgtgtgtgtaacctatagagcaaccccaagtttggacacttgaaatc	924
QY	781	acgacagatctctgtatacaatttcacgtgttaacagaagttgtgtgtggggagatgaacccgcgt	840
Db	925	acgacagatctctgtatacaatttcacgtgttaacagaagttgtgtgtggggagatgaacccgcgt	984
QY	841	ccaatttcaatctgttactctgtgaaacacagagaatgtggccaagtccctctggccgagcgtgc	900
Db	985	ccaatttcaatctgttactctgtgaaacacagagaatgtggccaagtccctctggccgagcgtgc	1044
QY	901	tttagagcccgagctgtgtctgtgccccaggaagaagacagaaagcggatgaaagatagcacc	960

Db 1045 tttagagccggatctgcttgccagagagacaggaagcgagatgaatagcattc 1104
QY 961 agaaagcagcaagtttcgcagcagtaacaagaacggtgtagtgcagagccgcttcgt 1020
Db 1105 agaaagcagcaagtttcgcagcagtaacaagaacggtgtagtgcagagccgcttcgt 1164
QY 1021 cagaacacatgtagtgcagcagtaacaacatcacaagaagaagatcccgatgatgaa 1080
Db 1165 cagaacacacatgtagtgcagcagtaacaacatcacaagaagaagatcccgatgatgaa 1224
QY 1081 ctgttactactacagtgagggcgctgagactatgaaatgctgttgaagatcaagaag 1140
Db 1225 ctgttactactacagtgagggcgctgagactatgaaatgctgttgaagatcaagaag 1284
QY 1141 tccctggaactatgcagtagtacctctccagcacacaattgaacgtagcaggaacaa 1200
Db 1285 tccctggaactatgcagtagtacctctccagcacacaattgaacgtagcaggaacaa 1344
QY 1201 cagcagcagcagcagcagcactactcagaaga 1232
Db 1345 cagcagcagcagcagcagcactactcagaaga 1376

RESULT 8

AAC66028.

ID AAC66028 standard; cDNA; 2270 BP.

XX AAC66028;

DT 21-FEB-2001 (first entry)

DE Human lung cancer-associated cDNA p63 isoform 2.

KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
vaccine; detection; ss.

XX Homo sapiens.

XX MO200061612-A2.

PD 19-OCT-2000.

PF 03-APR-2000; 2000MO-US08896.

PR 02-APR-1999; 9905-0285479.

PR 17-DEC-1999; 9905-0466396.

PR 30-DEC-1999; 9905-0476496.

PR 10-JAN-2000; 2000US-0480884.

PR 22-FEB-2000; 2000US-0510376.

PA (CORI-) CORIXA CORP.

PI Wang T, Fan L;

DR MPI: 2000-628399/60.

XX P-PSDB; AAB11358.

XX

PS Claim 25a; Page 237-238; 261pp; English.

CC This invention describes a novel isolated polypeptide (I) which
CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
CC which have cytostatic activity. The polypeptides and polynucleotides are
CC used in compositions and vaccines to inhibit the development of cancer,
CC especially lung cancer, in a patient. Methods described in the invention
CC can be used to monitor the progression of a cancer by carrying out the
CC detection at subsequent time points and comparing the results from the
CC different time points. CD4+ and/or CD8+ T-Cells isolated from a patient
CC are treated with P2, polynucleotides encoding P2 or antigen presenting
CC cells expressing P2 and then administered to the patient to inhibit

CC development of cancer.

XX Sequence 2270 BP; 595 A; 676 C; 501 G; 498 T; 0 other;

Query Match 91.7%; Score 1232; DB 21; Length 2270;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtccagagcacacagacaatgaaatctccagtcagaggtttccagcatatcgtg 60
Db 145 atgtccagagcacacagacaatgaaatctccagtcagaggtttccagcatatcgtg 204
QY 61 gattttctggaacagcctatatgttcagttccagccattgacttgaacttggggatgaa 120
Db 205 gattttctggaacagcctatatgttcagttccagccattgacttgaacttggggatgaa 264
QY 121 ccatcagaagatggtgcagacaacaagattgagattgagctgagctgtatccgcatgag 180
Db 265 ccatcagaagatggtgcagacaacaagattgagattgagctgagctgtatccgcatgag 324
QY 181 gactcgagcctgagtgagcccatgtggtccacagttacacagaaacttgggtctctgaacagc 240
Db 325 gactcgagcctgagtgagcccatgtggtccacagttacacagaaacttgggtctctgaacagc 384
QY 241 atgagcagcagagatcagaacagcgtcctgtccacagatccctataacacagaccagcg 300
Db 385 atgagcagcagagatcagaacagcgtcctgtccacagatccctataacacagaccagcg 444
QY 301 cagaacagcgtcagcagcgtcctgtccacagcagcagcagcagcagcagcagcagcagcagc 360
Db 445 cagaacagcgtcagcagcgtcctgtccacagcagcagcagcagcagcagcagcagcagcagc 504
QY 361 tctccatccaccggtccatccctccacacagcagcagcagcagcagcagcagcagcagcagcagc 420
Db 505 tctccatccaccggtccatccctccacacagcagcagcagcagcagcagcagcagcagcagcagc 564
QY 421 tccctccagcagtcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 480
Db 565 tccctccagcagtcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 624
QY 481 aaactctactgccaatattgaaagacatgcccacatccagaatcaaggtgagacccaccc 540
Db 625 aaactctactgccaatattgaaagacatgcccacatccagaatcaaggtgagacccaccc 684
QY 541 cctcagagcagcgtgtatccgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 600
Db 685 cctcagagcagcgtgtatccgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 744
QY 601 gtgtgtagagcgtgtgcccacacatgagctgagccgtgaaattcaacagagagcagattgcc 660
Db 745 gtgtgtagagcgtgtgcccacacatgagctgagccgtgaaattcaacagagagcagattgcc 804
QY 661 cctcctgattcattgtatgtagtagagggagagagcagcagcagcagcagcagcagcagcagcagc 720
Db 805 cctcctgattcattgtatgtagtagagggagagagcagcagcagcagcagcagcagcagcagcagc 864
QY 721 atcaacagagacagagtggtgcgtgtagcctatgagcagcagcagcagcagcagcagcagcagcagc 780
Db 865 atcaacagagacagagtggtgcgtgtagcctatgagcagcagcagcagcagcagcagcagcagcagc 924
QY 781 acgacagcttgttaacaattcaatgtagtaacagagtgtagtgtagagagtagaaccgcgt 840
Db 925 acgacagcttgttaacaattcaatgtagtaacagagtgtagtgtagagagtagaaccgcgt 984
QY 841 ccaatttaactatgttgaatctggaacacagagatggaagatccctgggagcagagctgc 900
Db 985 ccaatttaactatgttgaatctggaacacagagatggaagatccctgggagcagagctgc 1044
QY 901 tttagagcccgagatctgtctgtccagagagagacagagcagagcagagtagaagtagaagcagc 960
Db 1045 tttagagcccgagatctgtctgtccagagagagacagagcagagcagagtagaagtagaagcagc 1104

QY 961 agaaagcagcaagtttcgacagctacaaagaacggtgatgtatcagaagcggcgttcgt 1020
 Db 1105 agaaagcagcaagtttcgacagctacaaagaacggtgatgtatcagaagcggcgttcgt 1164
 QY 1021 cagaacacatcgtatccagatgatccatcaagaacggaagttcccgatgatgaa 1080
 Db 1165 cagaacacatcgtatccagatgatccatcaagaacggaagttcccgatgatgaa 1224
 QY 1081 ctgttactactacagtgagggcggtgagactatgtaatgctgttgaagaatcaagag 1140
 Db 1225 ctgttactactacagtgagggcggtgagactatgtaatgctgttgaagaatcaagag 1284
 QY 1141 tcccttgaaactatgacgaccccttcacagacaaattgaaacgtatcaggaacagaa 1200
 Db 1285 tcccttgaaactatgacgaccccttcacagacaaattgaaacgtatcaggaacagaa 1344
 QY 1201 cagcagcagcaccacacttacttactaagaaca 1232
 Db 1345 cagcagcagcaccacacttacttactaagaaca 1376

RESULT 9

AAZ43913

ID AAZ43913 standard; cDNA; 4846 BP.

AC AAZ43913:

DT 14-MAR-2000 (first entry)

XX Human KET cDNA.

XX KET; anticancer; cell cycle; apoptosis; tumor suppressor; p53 family;

XX p53 family; angiogenic; cytotoxic; cancer; human; ss.

OS Homo sapiens.

XX WO961610-A2.

XX 02-DEC-1999.

XX 25-MAY-1999; 99WO-DE01557.

XX 25-MAY-1998; 98DE-1022985.

XX (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.

XX Paul D, Augustin M, Schmale H, Bamberger C;

XX MPI; 2000-062710/05.

XX P-PSDB; AAY50997.

XX New KET-encoding nucleic acid and related proteins, for diagnosis and

XX treatment of tumors -

XX Claim 3; Page 23-26; 28pp; German.

XX This invention describes a novel KET-encoding nucleic acid (I) and its
 CC fragments, variants and mutants which has anticancer activity. (I)
 CC encodes a protein, (II), involved in control of the cell cycle and
 CC apoptosis, i.e. (II) is a tumor suppressor protein which belongs to the
 CC p53 family. (I), and the polypeptide (II) encoded by it, are used (a) to
 CC detect (I) in biological samples, specifically angiogenic tumor tissue,
 CC including (I) sequences that have a homozygotic deletion and (b) to
 CC detect presence or absence of human chromosome 3q27 or murine chromosome
 CC 16, or their fragments, by hybridization. Also, (I) is used as a tumor
 CC suppressor, particularly in tumors where an alteration in the wild-type
 CC p53 allele has not been identified. (I) and (II) may also be used for
 CC development of specific cytotoxic agents and for predicting the risk of
 CC developing cancer. This sequence represents the human KET cDNA sequence
 CC described in the method of the invention.

XX Sequence 4846 BP; 1372 A; 1077 C; 990 G; 1406 T; 1 other;

Query Match 91.7%; Score 1232; DB 21; Length 4846;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgtccagagcacacacagacaatgaattcctcagtcagaggttttcagcatatcgg 60
 Db 145 atgtccagagcacacacagacaatgaattcctcagtcagaggttttcagcatatcgg 204
 QY 61 gatttcggaagacgctatatatgttcagttccagccattgacttgaacttggatgaa 120
 Db 205 gatttcggaagacgctatatatgttcagttccagccattgacttgaacttggatgaa 264
 QY 121 ccattcagaagaatgtgtgcacaacaagaattgagatgattgactgtatccgcag 180
 Db 265 ccattcagaagaatgtgtgcacaacaagaattgagatgattgactgtatccgcag 324
 QY 181 gactcgacgtgagtgaccccatgtgtgcacagatcacagacctggggtctctgaagc 240
 Db 325 gactcgacgtgagtgaccccatgtgtgcacagatcacagacctggggtctctgaagc 384
 QY 241 atgagcagcagatgacagacgctcctcgtccacagttccctataacagacacgcg 300
 Db 385 atgagcagcagatgacagacgctcctcgtccacagttccctataacagacacgcg 444
 QY 301 cagaacagcgtacagcgccctcgtccacagacagcagcagcagcagcagcagcagc 444
 Db 445 cagaacagcgtacagcgccctcgtccacagacagcagcagcagcagcagcagcagc 504
 QY 361 tctcatatacccgccatccctcccaacacagcagcagcagcagcagcagcagcagc 504
 Db 505 tctcatatacccgccatccctcccaacacagcagcagcagcagcagcagcagcagc 564
 QY 421 tccctccagcagtcgagacccgacagtcgacccctgagcagtcattccactgaag 480
 Db 565 tccctccagcagtcgagacccgacagtcgacccctgagcagtcattccactgaag 624
 QY 481 aaactctactgccaatttcgaagaacatgcccacatccagatcaagtgatgacccact 540
 Db 625 aaactctactgccaatttcgaagaacatgcccacatccagatcaagtgatgacccact 684
 QY 541 cctcagggagcgtgtatccgcgcacatgctgtctacaaaagaagctgagcagtcagag 600
 Db 685 cctcagggagcgtgtatccgcgcacatgctgtctacaaaagaagctgagcagtcagag 744
 QY 601 gtgtgaagcgtgtgcccacaacatgagctgagcgtgtaattcaacggaaggacattgac 660
 Db 745 gtgtgaagcgtgtgcccacaacatgagctgagcgtgtaattcaacggaaggacattgac 804
 QY 661 cctcctagtcattgtatcgaatgaggggaacagccatccagatgtagaagatccc 720
 Db 805 cctcctagtcattgtatcgaatgaggggaacagccatccagatgtagaagatccc 864
 QY 721 atcacaggaagacagagtgctggtacattatgagccacccaggttggcactgattac 780
 Db 865 atcacaggaagacagagtgctggtacattatgagccacccaggttggcactgattac 924
 QY 781 agcagacgtctgtacaatttcatgtatgaacagcgtgtgttgaaggatgaacgcgcgt 840
 Db 925 agcagacgtctgtacaatttcatgtatgaacagcgtgtgttgaaggatgaacgcgcgt 984
 QY 841 ccaatttaacatctgtactctgtgaaacagagatggtggaagctcgtggcagagcgcgc 900
 Db 985 ccaatttaacatctgtactctgtgaaacagagatggtggaagctcgtggcagagcgcgc 1044
 QY 901 tttagagccgagatcgtgtgttccaggaagagagaagagcgtgagatgaagcattc 960
 Db 1045 tttagagccgagatcgtgtgttccaggaagagagaagagcgtgagatgaagcattc 1104
 QY 961 agaaagcagcaagtttcgacagctacaaagaacggtgatgtatcagaagcggcgttcgt 1020
 Db 1105 agaaagcagcaagtttcgacagctacaaagaacggtgatgtatcagaagcggcgttcgt 1164

Db	1165	cagaacacacactggtatccagatgacatccatcaagaagaagatcccagatgatga	1222
Qy	1081	ctgtataactattaccagtagagggccgagagactatgaagaatgctgtttgaagtcagaag	1140
Db	1225	ctgtataactattaccagtagagggccgagagactatgaagaatgctgtttgaagtcagaag	1284
Qy	1141	tcctctggaactatgcagctactcttcctcagcacacaattgaaacgtacaggcaacagaa	1200
Db	1285	tcctctggaactatgcagctactcttcctcagcacacaattgaaacgtacaggcaacagaa	1344
Qy	1201	cagcagcagcaccagcacttacttcgaaga	1232
Db	1345	cagcagcagcaccagcacttacttcgaaga	1376

p63 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AA059531-64), polynucleotides (see AKX5872-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.

Sequence 1182 BP; 330 A; 342 C; 276 G; 234 T; 0 other.

Query Match	84.9%;	Score 1140.6;	DB 20;	Length 1182;
Best Local Similarity	98.4%;	Pred. No. 0;		
Matches 1152; Conservative	0;	Mismatches 19.	Indels 0.	Score 1140.6;

[illegible]


```

QY 541 cctcagagagctgtatccgcgcacatgctcgttactaacaagaacgtgagcagcagag 600
Db 658 ccacagagcgctgtatccgcgcacatgctcgttactaacaagaacgtgagcagcagag 717
QY 601 gtgttgagcggtgtcccaacacatgagctgagcgtgtaactcaagagagacagatgc 660
Db 718 gtgttgagacgaltccctaaccatgagctgagcgtgtaactcaagagagacagatgc 777
QY 661 cctcctagatcattgattcagtagaggggaaacacacatgcccagatgtagaagaatccc 720
Db 778 cctccagatcattcagtagaggggaaacacacatgcccagatgtagaagaatccc 837
QY 721 atcacagagagagagagtgctgctgtaactttagagccccacacaggttggcactaattc 780
Db 838 atcacagagagagagagtgctgctgtaactttagagccccacacaggttggcactaattc 897
QY 781 acgacagctctgtaacatttactgtgtaacagcagctgtgtgtgagggagatgaaccgcgt 840
Db 898 acgacagctctgtaacatttactgtgtaacagcagctgtgtgtgagggagatgaaccgcgt 957
QY 841 ccaatttaatactgtaactctgtaacacacagagatggcagatctctggccgacgtgc 900
Db 958 ccaatttaatactgtaactctgtaacacacagagatggcagatctctggccgacgtgc 1017
QY 901 ttgtgagggccgagatctgtgctgtgcccagagagagagagagagagagagatgagatagatc 960
Db 1018 ttgtgagggccgagatctgtgctgtgcccagagagagagagagagagagagatgagatagatc 1077
QY 961 agaaagcagcagagtgctcgagacagtaacagagcgtgtaagtgaagagcgccgcttcgt 1020
Db 1078 agaaagcagcagagtgctcgagacagtaacagagcgtgtaagtgaagagcgccgcttcgt 1125
QY 1021 cagaacacacagtgatcacaatgacatccatcaagaagaacagatccacagatgtgaa 1080
Db 1126 cagaacacacagtgatcacaatgacatccatcaagaagaacagatccacagatgtgaa 1185
QY 1081 ctgtatacttaccagtgagggcgctgagactatgaatgctgtgttgaaatcaagaag 1140
Db 1186 ctgtgtgttaccacagtgagggcgctgagactatgaatgctgtgttgaaatcaagaag 1245
QY 1141 tcctgtgaacacagtgatcacaatgacatccatcaagaagaacagatccacagatgtgaa 1200
Db 1246 tcactgtgagmcaatgacagtaactcctccacagacacagatcgaaacgtaacgacagcagc 1305
QY 1201 cagcagacagacacagcacttactcagaacacatctctctgagccgtctcagagatgag 1260
Db 1306 cagcagacagacacagcacttactcagaacacatctctctgagccgtctcagagatgag 1365
QY 1261 ctgtgagagcccgagagagaactccaacaacatctgacgtctctttagaatccaaag 1320
Db 1366 ctgtgtgagagcccgagagagaactccaacaacatctgacgtctctttagaatccaaag 1425
QY 1321 cccccaacacgcatcagtgatcca 1344
Db 1426 cccccaacacacatcgtgatacca 1449

```

RESULT 13
AAK58577
ID AAK58577 standard; cDNA; 2043 BP.

XX AAK58577;
XX
XX 16-AUG-1999 (first entry)
DE Human cell regulatory protein p63, isoform deltaNp63 gamma, cDNA.
XX
XX Cell regulatory protein; p63; hu-deltaNp63 gamma; human;
KM cancer; tumour suppressor; cell cycle control; apoptosis;
KW cell proliferation; cell differentiation; therapy; ss.
XX
OS Homo sapiens.

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XX  
PM W09919357-A2.  
XX  
PD 22-APR-1999.  
XX  
XX 02-OCT-1998; 98MO-US21992.  
PF  
PR 29-MAY-1998; 98US-0087216.  
PR 15-OCT-1997; 97US-0062076.  
XX  
PA (HARD ) HARVARD COLLEGE.  
PI  
PI McKeon F, Yang A;  
XX  
XX WPI: 1999-277595/23.  
DR P-PSDB: AAT05958.  
PT  
PT New isolated p63 cell regulatory protein for, e.g. treatment of  
PS tumours  
PS  
PS Claim 1: Fig 14; 161pp; English.

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The present invention concerns the discovery of a new family of cell regulatory proteins (CRPs) termed the p63 family of proteins, which demonstrate certain sequence identity to known tumour suppressor proteins p53 and p73. It has been observed that the intron-exon organisation is conserved between p73 and p53, and from known exon and intron sizes for these 2 genes. It was possible to identify new members of this gene family using a PCR-based strategy of amplifying 2 exons in a conserved domain and their intervening intron. The human p53 gene was localised to chromosomal position 3q27-29. At least 6 different isoforms exist. Splice variants differing at the C-terminus have been designated as alpha, beta and gamma forms, while p63 members have been designated as delta and epsilon, where the delta form lacks the transactivation domain. The present sequence represents a cDNA clone encoding human deltaNp63 gamma. p63 was detected in a variety of human and mouse tissue. It demonstrates remarkably divergent activities, such as the ability to transactivate p53 reporter genes and induce apoptosis. Cessation or down-regulation of p53 expression may play a critical role in the process of cervical squamous cell differentiation, both benign and neoplastic. DeltaN isoforms of p63 act as dominant negatives towards transactivation by p53 and p63. p63 may also be implicated in haematopoiesis, muscle wasting (e.g. cachexia) and neuronal differentiation and related degenerative disorders. p63 polypeptides (see AY05953-64), polynucleotides (see AAK58572-83) and anti-p63 antibodies of the invention can be used to identify compounds useful for treating disorders involving such processes, in detection and diagnosis, and in the production of transgenic animals.

Sequence 2043 BP; 536 A; 623 C; 471 G; 413 T; 0 other;

Query Match 78.8%; Score 1059.2; DB 20; Length 2043;
Best Local Similarity 91.2%; Pred. No. 0;
Matches 1124; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
QY 1 atgtccacagacacacagacacatgaattctctcagtcagagaggttccagcatatcg 60
Db 118 atgtccagagagacacacagacacagagtcctcagccagaggtctccagcatatcg 177
QY 61 gatttctggaacacgctatattgttcagttcagccattgactgaacttggatgaa 120
Db 178 gatttctggaacacgctatattgttcagttcagccattgactgaacttggatgaa 237
QY 121 ccatcagaagatggtggagacaacaagaattgagattagacatgagacttccgcagcag 180
Db 238 ccttcgcgaatgtgtcacaacaagaattgagattagacatgagacttccgcagcag 297
QY 181 gactcgaactgagaccacatgtgcccacagttacacgaacctgggctctcgaacagc 240
Db 298 gactcgaactcagtgaccccatgtgcccacagttacacgaacctgggctctcgaacagc 357

```

QY 241 atgacacagatgacagagcgtctcgtccaccagttccctataacagacagcgc 300
DB 358 atgaccacagagatcctacagagcgtcctcgtccaccagccctacacacagcgc 417
QY 301 cagaacagctcagcgcgcctcgcctacagcagccacgcctccactgctctc 360
DB 418 cagaatagcgtgacgcgcctcgcctacagcagccacgcctccactgctctc 477
QY 361 tctcaccacgcgcctcctccacacagcactaccagccgcgcgcagttcgacgt 420
DB 478 tctcaccacgcgcctcctccacacagcactaccagccgcgcgcagttcgacgt 537
QY 421 tcttcacagcagtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 480
DB 538 tcttcacagcagtcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 597
QY 481 aaactcactgcacaaattgcaagacatgcccacatccagatcgaagtgatgacccac 540
DB 598 aagctgactgcacagatctgcgaagacatgcccacatccagatcgaagtgatgacccac 657
QY 541 cctcagggagctgtatccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 600
DB 658 ccaacagggcgcgtgtatccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 717
QY 601 gctgtgaacgcgtgcccacacatgagcgtgagcgtgaatcaacagggagcagatgac 660
DB 718 gctgtgaacgcgtgcccacacatgagcgtgagcgtgaatcaacagggagcagatgac 777
QY 661 cctccagcattgtatctgagtagaggggaacagcattccagcattgagagatccc 720
DB 778 cctccagcattgtatctgagtagaggggaacagcattccagcattgagagatccc 837
QY 721 atcacaggaagacagagctgtctgtacacctatgagccacccaggcttggcattgattc 780
DB 838 atcacaggaagacagagcgtgtctgtacacctatgagccacccaggcttggcattgattc 897
QY 781 agcagcgtcttgcacattcattgattgattgattgattgattgattgattgattgatt 840
DB 898 acacagcgtcttgcacattcattgattgattgattgattgattgattgattgattgatt 957
QY 841 ccaatttaacatctgtactcgtgaaacacagagatggggaagctccctggcgacagctgc 900
DB 958 ccaatttaacatctgtactcgtgaaacacagagatggggaagctccctggcgacagctgc 1017
QY 901 ttgagagcccgagctgtctgtctgcccaggaagacagagagcgagtgagaatgacatc 960
DB 1018 ttgagagcccgagctgtctgtctgcccaggaagacagagagcgagtgagaatgacatc 1077
QY 961 agaaagcagcagatcttcgagacgtacaaagaagcgtgattgattgattgattgatt 1020
DB 1078 agaaagcagcagatcttcgagacgtacaaagaagcgtgattgattgattgattgatt 1137
QY 1021 cagaacacacatggtatcagatgacatccatcaagaagaagatcccccagatgattgaa 1080
DB 1138 cagaacacacatggtatcagatgacatccatcaagaagaagatcccccagatgattgaa 1197
QY 1081 cgttatactacacagtgagggcgctgagactatgaaatgctgttgaagatcaagaag 1140
DB 1198 cgttatactacacagtgagggcgctgagactatgaaatgctgttgaagatcaagaag 1257
QY 1141 tccctggaactcattgacatcttctcagacacaaatggaacgtacaggaacagcaa 1200
DB 1258 tccctggaactcattgacatcttctcagacacaaatggaacgtacaggaacagcaa 1317
QY 1201 cagcagcagcagcagcactactactcagaaca 1232
DB 1318 cagcagcagcagcagcactactactcagaaca 1349

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RESULT 14
AA227674
ID AA227674 standard; DNA; 2082 BP.

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XX AC AA227674;
XX XX
XX 20-DEC-1999 (first entry)
XX DT
XX DE Human p40 coding sequence.
XX DE
XX KW Human; p40; p53 homologue; oncogene; diagnosis; proliferative disease;
XX KW anticancer therapeutic identification; cancer; immunogen; neoplasia;
XX KW Immunoblotting reagent; tumour; dysplasia; hyperplasia; therapy; ss.
XX OS Homo sapiens.
XX PN MO950287-A2.
XX PD 07-OCT-1999.
XX XX
XX 26-MAR-1999; 99MO-US06657.
XX PR 27-MAR-1998; 98US-0079736.
XX XX
XX (UYJO ) UNITV JOHNS HOPKINS.
XX PI Trink B, Jen J, Ratovitski E, Sidransky D;
XX DR WPI, 1999-591272/50.
XX DR P-PDB; AAY43135.
XX PT Isolated oncoproteins used to classify and diagnose tumours, and in
XX PT screens for identifying anticancer agents -
XX PS Claim 6; Page 58-59; 63pp: English.
XX XX
XX CC This sequence encodes the human p40 protein of the invention. p40 (the
XX CC shortest variant of a new human p53 homologue) is oncogenic and detection
XX CC of its overexpression (at protein or nucleic acid levels) is used to
XX CC diagnose and classify cancers or other proliferative diseases. It can
XX CC also be used to identify agents, potential anticancer therapeutics, that
XX CC modulates its binding to p53. p40 (or its fragments or fusion proteins)
XX CC are used as immunogens to raise (or to purify) antibodies. Antibodies are
XX CC used as immunosays reagents for detecting overexpression of p40, also
XX CC therapeutically against tumours. Fragments of the nucleic acid that
XX CC encode p40 are used for recombinant expression; as probes to quantify p40
XX CC gene expression or to identify related sequences; also chromosome 3q.
XX CC Antisense fragments are useful for inhibiting expression of p40, for
XX CC treatment of neoplasia, dysplasia and hyperplasia.
XX CC
XX SO Sequence 2082 BP; 605 A; 493 C; 473 G; 511 T; 0 other;

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Query Match 76.7%; Score 1031.2; DB 20; Length 2082;
Best Local Similarity 95.7%; Pred. No. 4.2e-292;
Matches 1060; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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QY 125 cagaagatggtgacaaagaagatgagtagatgacgtatccagatgcagact 184
DB 395 cagaagaaagagacagacagatgattcattacagcactacatggttactggaagaac 454
QY 185 cgaacgtgagtgaccccatgtgcccacagtacagacagctggggtcctgtaacagatgg 244
DB 455 atgccagactcaatttagtgagcaagtaacagacagcactgggggtcctcgaagaagatgg 514
QY 245 atccagagattcgaagcgtcctcgtccacagctccctataacacagacagcgcagaga 304
DB 515 accagagattcagaacggtcctcgtccacagctccctataacacagacagcgcagaga 574
QY 305 acagcgtacagcgcgcctcgcctcgaacagacagcagctccacttcgagctctcttc 364
DB 575 acagcgtacagcgcgcctcgcctcgaacagacagcagctccacttcgagctctcttc 634
QY 365 catcacccgcacatccctccaaacacagcactaccagccgcgcagcttcgagctgctct 424
DB 635 catcacccgcacatccctccaaacacagcactaccagccgcgcagcttcgagctgctct 694

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QY 425 tccagcagtcgagcaaccgcaagtcgcccacgtgagctatctccactgaaagaac 484
 Db 695 tccagcagtcgagcaaccgcaagtcgcccacgtgagctatctccactgaaagaac 754
 QY 485 tctactgccaatctgcaagaacatgcccacatccagatcaagtgatgacccactctc 544
 Db 755 tctactgccaatctgcaagaacatgcccacatccagatcaagtgatgacccactctc 814
 QY 545 agggagctgtatccgcgcctgctctctacaaaagctgagcaagtcagagagtg 604
 Db 815 agggagctgtatccgcgcctgctctctacaaaagctgagcaagtcagagagtg 874
 QY 605 tgaagcgtgcccacacacatgagctgagccgtgaaatcaacgagagagagtgccctc 664
 Db 875 tgaagcgtgcccacacacatgagctgagccgtgaaatcaacgagagagagtgccctc 934
 QY 665 ctatgcatctgagtcgagtagagggagagacagctgcccagatgtagaagaatccatca 724
 Db 935 ctatgcatctgagtcgagtagagggagagacagctgcccagatgtagaagaatccatca 994
 QY 725 caggagaacagagtgctgctgtacccatgagccacccagcttgagcaatcaacga 784
 Db 995 caggagaacagagtgctgctgtacccatgagccacccagcttgagcaatcaacga 1054
 QY 785 cagctctgtacaaatctcatgctgtaacagagctgtgtgagagagtagaacgcgtccaa 844
 Db 1055 cagctctgtacaaatctcatgctgtaacagagctgtgtgagagagtagaacgcgtccaa 1114
 QY 845 tttaatactgttactctggaacacagagatgagcaagctcctgagcagagctgtctg 904
 Db 1115 tttaatactgttactctggaacacagagatgagcaagctcctgagcagagctgtctg 1174
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 Db 1175 aggcgcgcgtcgtctgtgcccagagaagacagagagcgagatgaaagatagatcaaga 1234
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 Db 1235 agcagcaagcttctgcaagctacaaagaacggtgagtagcgaagcgcgtcttcgacaa 1294
 QY 1025 acacacatgctatccagatgacatccatcaagaacagaaatccacagatgaaagtgt 1084
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 Db 1415 tggaaactatgagtaacctctcagcacacacatgaaacgtaacgagcaacagcagc 1474
 QY 1205 agcagcagcagcagctactactcagaaca 1232
 Db 1475 agcagcagcagcagctactactcagaaca 1502

RESULT 15
 AAC66030
 ID AAC66030 standard; cDNA; 2082 BP.

AC AAC66030;
 XX
 XX 21-FEB-2001 (first entry)

DE Human lung cancer-associated cDNA p63 isoform 4.

KW Lung cancer; therapy; treatment; human; tumor; immunogenic; cytostatic;
 KM vaccine; detection; ss.
 OS
 XX Homo sapiens.

PN WO200061612-A2.
 PD 19-OCT-2000.
 XX
 PF 03-APR-2000; 2000MO-US08896.
 XX
 PR 02-APR-1999; 9905-0285479.
 PR 17-DEC-1999; 9905-0466396.
 PR 30-DEC-1999; 9905-0476496.
 PR 10-JAN-2000; 2000US-0480884.
 PR 22-FEB-2000; 2000US-0510376.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Wang T, Fan L;
 XX
 DR WPI; 2000-628399/60.
 DR P-PSDB; AAB11360.
 XX
 PT Isolated polypeptide comprising an immunogenic portion of a lung tumor
 XX protein is used for detecting and monitoring progression of lung cancer
 PS in a patient -
 XX
 PS Claim 25a; Page 239-240; 261pp; English.
 CC
 CC This invention describes a novel isolated polypeptide (I) which
 CC comprising an immunogenic portion of a lung tumor protein or variant (P2)
 CC which have cytostatic activity. The polypeptides and polynucleotides are
 CC used in compositions and vaccines to inhibit the development of cancer,
 CC especially lung cancer, in a patient. Methods described in the invention
 CC can be used to monitor the progression of a cancer by carrying out the
 CC detection at subsequent time points and comparing the results from the
 CC different time points. CD4+ and/or CD8+ T-cells isolated from a patient
 CC are treated with P2, polynucleotides encoding P2 or antigen presenting
 CC cells expressing P2 and then administered to the patient to inhibit
 CC development of cancer.
 XX
 SQ Sequence 2082 BP; 605 A; 493 C; 473 G; 511 T; 0 other;

Query Match 76.7%; Score 1031.2; DB 21; Length 2082;
 Best Local Similarity 95.7%; Pred NO. 4.2e-292;
 Matches 1060; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
 QY 125 cagaagaatgttggaacaacaaagattgagatgagatgagctgataccgcatgagagact 184
 Db 395 cagaagaagaagaaagacagattgataatcttaacagtaacatgttgtaactgtaaaaca 454
 QY 185 cggactgagtgaccacatgctgacacagtaacagaacttgggtctcctgaagaacatgg 244
 Db 455 atgccagactcaatttagtgagccacagtaacacgaaccttgggtctcctgaagaacatgg 514
 QY 245 accagaagaattagaagaagctctcctgctacacagatccctataacacagacagcgcaga 304
 Db 515 accagaagaattagaagaagctctcctgctacacagatccctataacacagacagcgcaga 574
 QY 305 acagcgtacagcgccctcgcgcctcctacagacagacagccagctcactccatgctctctc 364
 Db 575 acagcgtacagcgccctcgcgcctcctacagacagacagccagctcactccatgctctctc 634
 QY 365 catcacccgcatccctccacaaacacgactacccacagcccgacagcttcgcagagtgctct 424
 Db 635 catcacccgcatccctccacaaacacgactacccacagcccgacagcttcgcagagtgctct 694
 QY 425 tccagcagtcgagcaccgcaagtcgcccacacgtgagcgtatccactgtaactggaagaac 484
 Db 695 tccagcagtcgagcaccgcaagtcgcccacacgtgagcgtatccactgtaactggaagaac 754
 QY 485 tctactgccaatctgcaagaacatgcccacatccagatcaagtgatgacccactctc 544
 Db 755 tctactgccaatctgcaagaacatgcccacatccagatcaagtgatgacccactctc 814
 QY 545 agggagctgtatccgcgcctgctctctacaaaagctgagcaagtcagagagtg 604


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Db 815 agggagcgttatccgcgcgcgtatccgtctacaaaaagctgagcacgtcacggaggtg 874
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Db 875 tgaagcgtgtccccaaccaatgagctgagcgttgaaatcaacgaggagacagattgccctc 934
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QY 665 ctatcatttattcgtgtagagggaacacatgcccagtatgtagaaatcccatca 724
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Db 935 ctatcatttattcgtgtagagggaacacatgcccagtatgtagaaatcccatca 994
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QY 725 caggaagacacagtgctgtgtgtacctaagcaccacaggttggcactgaattcacga 784
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Db 995 caggaagacacagtgctgtgtgtgtacctaagcaccacaggttggcactgaattcacga 1054
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|||
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Db 1115 tttaaatcattgttacctctggaacacagagatggcgaagtcctggccgacgtgcttg 1174
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QY 905 aggcccgatctgtgctgtgccaggaagacaggaagcgagatgaaatagcatcagaa 964
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QY 965 agcagcaagtttcggaacgtacaagaacggtgattgtacgaagcgcgcttcgtcaga 1024
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Db 1235 agcagcaagtttcggaacgtacaagaacggtgattgtacgaagcgcgcttcgtcaga 1294
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QY 1085 tatactaccagtgaggggccgtgagacttaagaatgctgttgaagaatcaaaagatccc 1144
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Db 1355 tatactaccagtgaggggccgtgagacttaagaatgctgttgaagaatcaaaagatccc 1414
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QY 1205 agcagcaccagacttacttcagaaca 1232
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Db 1475 agcagcaccagacttacttcagaaca 1502
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Job time: 4025 sec

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QY 422 ccttcagcagtcgagcagccgacgaatcgccacactgagcgtatctccactgaactgaaga 481
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Db 362 GCTTCTTGCATCTTGGGACAGCCAAAGCTGTGACTTGCACGTACTCCCTCCCTCCCAACA 421
QY 482 aactctactgcaaatctgcaagaacatgacatccagatcaagatgagatgacccactc 541
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Db 422 AGATGTTTGGCAACTGGCGAAGACCTGGCTGTGACAGCTGTGTTGATTCACACGCC 481
QY 542 ctcaagagatgtagtattcgcgcgcacatgcctgctctacaaaaagctgagcagctcagag 601
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 CGCCCGGACACCCCGCTCCGCGCATATGCTTCAACAGAGTACACAGCAGCATGAGGAG 541
QY 602 ttgtgaagcagtgcccaacacagatgagccggtgaattcaacagagagacagatggcc 661
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 TTGTGAGGCGCTGCCCCACCATGAGCGCTGCTCAGATAGCCATG-----GTCTGGGCC 595
QY 662 ctctcagtcattgattcagatgagatgagaggaagacatgcccagatgtagaagatccca 721
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Db 596 CTCTCAGCATCTTATCCAGTGGAGAAATTTGCGTGTGAGATTTGATGACAGAA 655
QY 722 tcacaggaagacagatgtgctgtagtacctatgagccacccagctgtagcactgaatca 781
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 656 ACACCTTTTGACATAGTGTGTGATCCTATGACCCGCTGAGGTGCTCTGACTGTGA 715
QY 782 cgacagctctgtaacaattcattgtagtaacagagctgtgttggagagatgaacccgctc 841
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Db 716 CCACCATTCACATCACTACATGATGTAAACAGTTCTGCTGATGGCGGATGAAACCGAG 775
QY 842 caatttaatactatgctctcgtgaacacagagatgagccagctgctgagccgagcgtgct 901
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 776 CCATCCTCCTACATCACTACATGAGAGACTCCATGAGTGAATCTGTGGAGAGGAAACGT 835
QY 902 ttgagcccgagatctgtgctgctgagcagaagagacagagagcgagatgagatagatca 961
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 836 TTGAGGTGCTGTGTTGTCTCTCTCTGGAGAGACCGCGCAGAGAGAGAGAAATCTCC 895
QY 962 gaaagcagcagatctcgagcagtagaagaacagatgtagtgaagacgcccgttctgctc 1021
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 896 GCAAGAAAGGGAGGCTCACCACAGACGCTCCCGCAGAGAGACATMAACGAGCACTGGCCA 955
QY 1022 agaacacatgtagtaccagatgacatccatcaagaagaacagatgtagtgaagatga 1081
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 956 ACAACAC-----CAGCTCTCTCCCAAGCCCAAGAAAGAAACCACTGATGAGAAAT 1006
QY 1082 tgtatactaccagtaggagccgtgagactatgaatgagctgtagaagataaagatg 1141
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1007 ATTTCACCTTCATATCCGGGGGCTGAGCGCTTCGAATGTTCCGAGAGCTGAATGAGG 1066
QY 1142 cccctggaactcagtagtacccttctcagca 1172
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1067 CCTTGAACCTCAAGAGATGCCAGGCTGGAA 1097

```

```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,357
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/347,792
FILING DATE: 28-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST580USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
FAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-431-357-20

Query Match      18.2%  Score 244.2: DB 1: Length 1215;
Best Local Similarity 58.3%  Pred. No. 5.5e-64;
Matches 473; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

QY 362 ctccacaccgcccacccctcccaaacacgactaccagagccgacagatctcgagctg 421
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 CCTGTGATCTTCTGTCTCTCCCTCCAGAAACCTACACAGGCGACGTACAGGTTCCGTCTG 361
QY 422 ccttcagcagtcgagcagccgacgaatcgccacactgagcgtatctccactgaactgaaga 481
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 GCTTCTTGCATCTTGGGACAGCCAAAGCTGTGACTTGCACGTACTCCCTCCCTCCCAACA 421
QY 482 aactctactgcaaatctgcaagaacatgacatccagatcaagatgagatgacccactc 541
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 AGATGTTTGGCAACTGGCGAAGACCTGGCTGTGACAGCTGTGTTGATTCACACGCC 481
QY 542 ctcaagagatgtagtattcgcgcgcacatgcctgctctacaaaaagctgagcagctcagag 601
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 CGCCCGGACACCCCGCTCCGCGCATATGCTTCAACAGAGTACACAGCAGCATGAGGAG 541
QY 602 ttgtgaagcagtgcccaacacagatgagccggtgaattcaacagagagacagatggcc 661
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 TTGTGAGGCGCTGCCCCACCATGAGCGCTGCTCAGATAGCCATG-----GTCTGGGCC 595
QY 662 ctctcagtcattgattcagatgagatgagaggaagacatgcccagatgtagaagatccca 721
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 596 CTCTCAGCATCTTATCCAGTGGAGAAATTTGCGTGTGAGATTTGATGACAGAA 655
QY 722 tcacaggaagacagatgtgctgtagtacctatgagccacccagctgtagcactgaatca 781
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 656 ACACCTTTTGACATAGTGTGTGATCCTATGACCCGCTGAGGTGCTCTGACTGTGA 715
QY 782 cgacagctctgtaacaattcattgtagtaacagagctgtgttggagagatgaacccgctc 841
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 716 CCACCATTCACATCACTACATGATGTAAACAGTTCTGCTGATGGCGGATGAAACCGAG 775
QY 842 caatttaatactatgctctcgtgaacacagatgagccagctgtagcactgaatca 901
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 776 CCATCCTCCTACATCACTACATGAGAGACTCCATGAGTGAATCTGTGGAGAGGAAACGT 835
QY 902 ttgagcccgagatctgtgctgctgagcagaagagacagagcgagatgagatagatca 961
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 836 TTGAGGTGCTGTGTTGTCTCTCTGGAGAGACCGCGCAGAGAGAGAGAAATCTCC 895
QY 962 gaaagcagcagatctcgagcagtagaagaacagatgtagtgaagacgcccgttctgctc 1021
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 896 GCAAGAAAGGGAGGCTCACCACAGACGCTCCCGCAGAGAGACATMAACGAGCACTGGCCA 955

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QY	1022	agaacaacatggtaccagattgacctccatcaagaacgaagatccccagttgtaac	1081
Db	956	ACAACAC-----CAGTCTCTCTCCCGACCANAGAAGAAACACTGGATTGAGAT	1006
QY	1082	tgttatacttaccagtgtagggcgctgagactatbaatgcgttgtgaagatcaaagt	1141
Db	1007	ATTTCACCCCTTCAGATCCGGGGGCGTGACGCCCTTCGAATTTCCGACAGCTGAATGAGG	1066
QY	1142	cctctgaactcatgctcagttacttcctccaaga	1172
Db	1067	CCTTGGAACTCAAGATGCCCACGCTGGGGA	1097

RESULT 3

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US-08-392-542-26
Sequence 26, Application US/08392542
Patent No. 6169073
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
APPLICANT: Hartwig, Wolfgang
TITLE OF INVENTION: Peptides and Peptidomimetics with
TITLE OF INVENTION: Structural Similarity to Human p53 That Activate p53
TITLE OF INVENTION: Function
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,542
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0406.48439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ. ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-392-542-26

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Query Match	18.28	Score 244.2	DB 4	Length 1215
Best Local Similarity	58.38	Pred. No. 5.5e-64		
Matches 473	Conservative 0	Mismatches 323	Indels 15	Gaps 2

QY	362	ctcatcaaccgcatcccccctcaaaacgagatcccagcgccgaagtctaaagt	421
Db	302	ccctgctatcttctgtcccttccagaaaacttccagggcagctaacggtttccgttcg	361
QY	422	ccctcagcagtcgacgaccgccaagtcgycgacccttgcagctatccactgaactgaa	481
Db	362	gcttcttgcatcttggggacaccgaagctctgacttgcagctactccctccctcaaca	421
QY	482	aacctactgcgaattgcagaagcattgcgcccatccagatcaagvtgaccccatc	541

Db	422	AGATGTTTGGCAACTGGCGAAMACCTGGCCCTGTGACGCTGGGGTTGATTCACACGCC	481
Oy	542	ctcagggagctgltatctcggcgccatgcctgctcaacaaaaaactgagacgycacggagg	601
Db	482	CGCCCCGACCCCGCGTCCGGCCATGGCCCATCTACAGCACTCACAGCATGACGGAGG	541
Oy	602	tggfgaagcggtgcccacaacatgaaactgagccgtgtaattcaacagagagacagattggcc	661
Db	542	TTGGTAGGGCGGTGCCCCACCATGAGGGCGTCAATAGCATG-----GTCTGGGCC	595
Oy	662	ctctctagtcatttgattctcgagttagagggagacagccatgcccagatgtagaagaacca	721
Db	596	CTCCTCAGCAATCTTATCCGATCGATGGAAAGAAATTTGCTGTGGAGATTTGGATGACAGAA	655
Oy	722	tcacagaagaacagagatgtctgttaacctatgagccaccaggttggcaactgatatca	781
Db	656	ACACTTTTCACATAGTGTTGTTGGTACCCATGAGCGCGCTGAGGTTGGCTCTGACTGTA	715
Oy	782	cgacagctctgtacaattlcatatgtgtgaacagagctgtgtgtgagagatbaacgcgcgtc	841
Db	716	CCACCATTCACACTACAACTATCATGTGTGTAACAGTTCTCGATGGCGCGCATGAACCGAAGGC	775
Oy	842	caatttaatcatctgttacctctggaacacagagatbgygaagtcctctggcccgagctcct	901
Db	776	CCATCTCTACCATCATATACACTGGAAGACTCCAGTGTGTAATTACTGGGACCGAACA	835
Oy	902	ttagagcccgagatctgtctgtctgcgcagagaaagacacagaaagccgagatbaagatagcatca	961
Db	836	TTGAGGTGGCGTGTGTGGCTGTCTGTGGAGAGACCGCGCGCACAGAGGAAGAAATCTCC	895
Oy	962	gaaaagcagcaagtttcggacagfatacaaaagaaggytgaatgtatcgaaagccgcgttctgc	1021
Db	896	GCAAGAAAGGGGAACCTCCACACAGAGCTCCCCCCACAGGAGCACTAAGCGAGCACTGCCCA	955
Oy	1022	agaacacacatgfatccagatgacatcatcaataagaacagaaatccccacagatgtagac	1081
Db	956	ACAACAC-----CAGTCTCTCTCCACGCAAGAAGAAACACACTGATGAGAGAT	1006
Oy	1082	tgttatcttaccagtgaagggccgtgagactatgaataatgcctgttgaagatcaaagagt	1141
Db	1007	ATTTCACCCCTTCAGATCCCGCGGCGTGAAGCGCTTCGAAATGTTCCAGAGAGCTGAATGAGG	1066
Oy	1142	cccttgaaactatgcaagtactctccccaagca	1172
Db	1067	CTTTGAACTCAAGATGCCACAGCTGGGAA	1097

RESULT 4

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US-08-894-327-26
? Sequence 26, Application US/08894327
? Patent No. 6245886
? GENERAL INFORMATION:
? APPLICANT: Halazonetis, Thanos
? APPLICANT: Hartwig, Wolfgang
? TITLE OF INVENTION: Peptides and peptidomimetics with
? TITLE OF INVENTION: structural similarity to human p53 that activate p53
? TITLE OF INVENTION: function
? FILE REFERENCE: 2973.19998
? CURRENT APPLICATION NUMBER: US/08/894,327
? CURRENT FILING DATE: 1997-12-04
? EARLIER APPLICATION NUMBER: pectus96/01555
? EARLIER FILING DATE: 1996-02-16
? EARLIER APPLICATION NUMBER: 08/392,542
? EARLIER FILING DATE: 1995-02-16
? NUMBER OF SEQ ID NOS: 35
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 26
? LENGTH: 1215
? TYPE: DNA
? ORGANISM: Homo sapiens
US-08-894-327-26

```

Query Match 18.2%; Score 244.2; DB 4; Length 1215;
 Best Local Similarity 58.3%; Pred. No. 5.5e-64;
 Matches 473; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

362 ctccatccaccgcatccctcccaaacaccgagcccgccagagtttcagcgt 421
 302 cccgtcattctcttccctcccaaacaccgagcccgccagagtttcagcgt 421
 422 cctccagcagtcgagcccgccagagtttcagcgtccgagtttcagcgt 361
 362 gctctctgattcttgagcccgccagagtttcagcgtccgagtttcagcgt 421
 482 aactctactgcaaatgtgcaagacatgcccacagagtttcagcgtccgagtttcagcgt 421
 422 agatgttctgcaaatgtgcaagacatgcccacagagtttcagcgtccgagtttcagcgt 421
 542 ctcaaggagcgtgtatccgagccatgcttctctcaaaaagcttgagccgagag 601
 482 cgcgcgagcagccgctgcgcgcagctgcatctcaagcagctacagcagcagagag 541
 602 tggtagagcgtgtgcccacacatgagctgagccgtgagttcaacagagagagatgcc 661
 542 ttgtgagcgtgtgcccacacatgagctgagccgtgagttcaacagagagagatgcc 661
 662 ctccatgatttgcagttcagagtagagagagagagagagagagagagagagagagag 721
 596 ctctcagcagcttaccgagtagagagagagagagagagagagagagagagagagagag 655
 722 tcacaggaagacagagtgctgtgtacattatgagccagccagagtttgagcagatca 781
 656 acactcttcagacatagtggtgtgtacattatgagccagagagagagagagagagagag 715
 782 cgacagctctgtacattatgagagagagagagagagagagagagagagagagagagag 841
 716 ccacacatccac 775
 842 caatttaattctgttactctgagacacagagagagagagagagagagagagagagagag 901
 776 ccatctcctccac 835
 902 ttgagagccgagatctgtctgtcccaagagagagagagagagagagagagagagagagag 961
 836 ttgagagcgt 895
 962 gaaagcagcagttctgagcagttacaaagagagagagagagagagagagagagagagag 1021
 896 gcaagaaag 955
 1022 agaacacacatgtagatgagatgagatgagatgagatgagatgagatgagatgagatgag 1081
 956 acaaacac-----cagctctctctcccaagcagagagagagagagagagagagagagag 1006
 1082 tgtatattacacagtgagagcgtgtgagatgagatgagatgagatgagatgagatgagatgag 1141
 1007 attcaccctctgagatcgagagcgtgtgagatgagatgagatgagatgagatgagatgagatgag 1066
 1142 cccctgagacatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgag 1066
 1067 ccttgagacatgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatgag 1097

RESULT 5
 PCT-US95-15353-20
 Sequence 20, Application PC/TUS9515353
 GENERAL INFORMATION:
 APPLICANT: The Wistar Institute of Anatomy
 APPLICANT: and Biology
 APPLICANT: Halazone, Phanos D.
 TITLE OF INVENTION: p53 Protein with Altered
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESSES:
 ADDRESS: Howson and Howson

STREET: Spring House Corporate Cntr., PO Box 457
 CITY: Spring House
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19477
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/15353
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/347,792
 FILING DATE: 28-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/431,357
 FILING DATE: 28-APR-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/456,623
 FILING DATE: 01-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Bak, Mary E.
 REGISTRATION NUMBER: 31,215
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-540-9206
 TELEFAX: 215-540-5818
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1215 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 PCT-US95-15353-20

Query Match 18.2%; Score 244.2; DB 5; Length 1215;
 Best Local Similarity 58.3%; Pred. No. 5.5e-64;
 Matches 473; Conservative 0; Mismatches 323; Indels 15; Gaps 2;

362 ctccatccaccgcatccctcccaaacaccgagcccgccagagtttcagcgt 421
 302 cccgtcattcttcttccctcccaaacaccgagcccgccagagtttcagcgt 361
 422 cctccagcagtcgagcccgccagagtttcagcgtccgagtttcagcgt 481
 362 gctctctgattcttgagcccgccagagtttcagcgtccgagtttcagcgt 421
 482 aactctactgcaaatgtgcaagacatgcccacagagtttcagcgtccgagtttcagcgt 541
 422 agatgttctgcaaatgtgcaagacatgcccacagagtttcagcgtccgagtttcagcgt 481
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 542 ttgtgagcgtgtgcccacacatgagctgagccgtgagttcaacagagagagatgcc 661
 662 ctccatgatttgcagttcagagtagagagagagagagagagagagagagagagagag 721
 596 ctctcagcagcttaccgagtagagagagagagagagagagagagagagagagagagag 655
 722 tcacaggaagacagagtgctgtgtacattatgagccagccagagtttgagcagatca 781
 656 acactcttcagacatagtggtgtgtacattatgagccagagagagagagagagagagag 715
 782 cgacagctctgtacattatgagagagagagagagagagagagagagagagagagagag 841

APPLICANT: Draetta, Giulio
TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Elliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/247,904B
FILING DATE: 23-MAY-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029, 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1181
US-08-247-904B-11

Query Match 18.1%; Score 242.6; DB 2; Length 1181;
Best Local Similarity 58.2%; Pred. No. 1.7e-63;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;
QY 362 ctccataccgcgcacccctcccaacacgcgacccagccgacgacgttcgaagtg 421
DB 275 CCGTCATCTTCGTGTCCTCCAGAAACCTACCAAGGCGACGCTTCCGCTCG 334
QY 422 cttccagcggtgagacgcgcgacgacgtcgccacgtgacgtatccactgaaga 481
DB 335 GCTTCTTGCACTGTGGAGACGCCAGCTGTGTGACGCTGACGTACTCCCTGCCCTCACA 394
QY 482 aactctactgccaattgcaagacatgcccacatccagtgcaagtgtatgacccac 541
DB 395 AGATGTTTGGCAATGGCCAGAACCTGCTGTGACGCTGTGGGTGATTCCACACCC 454
QY 542 ctcaaggagctgtatccgcgcacgtgctgtctacaaaagctgacgacgtcgaagg 601
DB 455 CGCCCGCACCCGCGTCCCGCATGGCCATCTACAAAGCAGTCAAGCAGCATGACGAG 514
QY 602 tgggaagcggtgcccccaacatgagcggtgagcggtgaattcaagaggaaagtggc 661
DB 515 TTGTGAGGGGCGTCCCGCCACATGAGCGCTGCTCAGATAGCGATG-----GTCTG 568
QY 662 ctctcagtaattgtatcgtagagagggaacagcatgcccagatgtagaatccca 721
DB 569 CTCCTCAGCATCTATCCGATGGAAGAAATTTCGCTGAGATATTGGATGACAGAA 628
QY 722 tcacaggaagaaaggtgtgctggtactatgagcaaccccaaggttggacgtgaatca 781
DB 629 ACACCTTTCGACATAGGTGGGTGGCTCTATGAGCCCGCTGAGGTTGGCTGACGTGA 688
QY 782 cgacagctgtgacaaattcatgtgttaacagcagttggtggaggatgaacgcgctc 841

DB 689 CCACCATCACTACATACATGTTACAGTCTCTGCATGGCGGCATGAACCGAGGC 748
QY 842 caatttaattatgttactctctgaaacagaga tgggaagtccttggccgacgtgct 901
DB 749 CCATCTCCACATCATACATGTAAGACTCCAGTGTATCTACTGAGGACGGAACAGCT 808
QY 902 tgaagcccgatctgtcttgcaggaagacaggaagcggaatgagaatgacatca 961
DB 809 TTGAGGTGCGTGTGTGCTGCTGGAGAGACCGCGCCACAGAGAAAGCAATCTCC 868
QY 962 gaaagcgcaagttcgagacgtacaaagaagtgatgttcgaagcgccgttctgc 1021
DB 869 GCAAGAAAGGGAGCTCACACAGACCTGCCCGAGGAGACACTAAGGAGACACTGCCCA 928
QY 1022 agaacacacatgtatccagatgacatcacaagaagaagatccccagatgtgac 1081
DB 929 ACAACAC-----CACCTCTCTCCCGACCAAGAAACCACTGATGGAGAAAT 979
QY 1082 tgtatacttaccagtgaggcggtgagactatgaatgtctgttgaagatcaagagt 1141
DB 980 ATTTACCCCTTACATCCCTGGGCGTGAGCGCTTCGAGTGTCCGAGACGTAATGAG 1039
QY 1142 ccctggaactcatgacgtaccttccctcagca 1172
DB 1040 CCTTGAACCTCAAGATGCCAGGCTGGGAA 1070

RESULT 8
US-08-767-942A-22
Sequence 22, Application US/08767942A
Patent No. 6068982
GENERAL INFORMATION:
APPLICANT: Nolte, Mark
APPLICANT: Chiu, M. Isabel
APPLICANT: Berlin, Vivian
APPLICANT: Damagnez, Veronique
APPLICANT: Draetta, Giulio
APPLICANT: Guillaume, Cottarel
TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,942A
FILING DATE: 17-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029, 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1181 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1179
US-08-767-942A-22

Query Match 18.1%; Score 242.6; DB 3; Length 1181;
 Best Local Similarity 58.2%; Pred. No. 1.7e-63;
 Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

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QY 362 ctccatcacccgcacatccctcccaacacagcagcagcccgacagtttcgaagtg 421
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DB 275 CCTGTGATCTTCTGTCCTTCCAGAAAACCTACAGAGGACCTGCTGCTGCTG 334
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 422 ccttccagcagtcgagacacacgaagtcgccccttggaagttatccacgaactgaaga 481
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 335 GCTTCTTGCACTTGTGGAGACGCCAAGTCTGTGACTTGACAGTACTGCTCCCTCAACA 394
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 482 aactctactgccaatgtgcaaaagacatgcccacatcaagatgtagtgaacccacac 541
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 395 AGATGTTTTCAGCACTGAGCCAGACCTGCTGAGAGTGTGGTGTGATTCACACACCC 454
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 542 ctcaagagagctgtatccgagcagtcgctgtctacaaaagctgagcagtgagag 601
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DB 455 CGCCCGGACCCCGCTCCGCGCATGCGCTACAGAGCTACAGACATGACAGAGG 514
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QY 602 tggtagagcgtgtcccaacacagtcgagcgtgaattcaacagagagacagattgccc 651
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DB 515 TTCTGAGGCGCTGCTCCCGACATGAGCGCTGCTACATGACGATG-----GTCTGCGCC 568
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 662 ctctcagtcattgtatctgagtagagagagacagcagtcagtcagtagaagatccca 721
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DB 569 CTCCTCAGCATCTTATCCGAGTGGAGAAATTTGCGTGTGAGTATTTGATGACAGAA 628
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QY 722 tcaagagagagagagagtagtgcgtgtaacctatgagacaccccgagttgagcagatca 781
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DB 629 ACACCTTTTGACACTATGCTGTGTGCTCCCTATATAGCGCGCTGAGGTTGCTTGACGTGA 688
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QY 782 cgcagagctctgtacaattatcatgtgtaacagcagctgtgtgtgagagagatgaacgcgctgc 841
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 689 CCACCATTCACATCACTACATGTGTACAGTTCCTGTCATGCGCGCATACCGGAGGC 748
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 842 caatttaattcatgttactctgtgaaacacagagatgagcagtcgtgagcgcagcgtgc 901
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DB 749 CCATCTCACCATCACTACACTGGAAGACTGCAGTGTATATCTACGTGGAGCAACGCT 808
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 902 ttgagagccgagatctgtctgcccagagagagacagagagcgagtagaagatgacatca 961
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DB 809 TTGAGGTGGCTGTTGTGTGCTGTCTGCGGAGACCGCGCCACAGAGGAGAAATCTCC 868
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QY 962 gaaagcagcagagttctggagcagtagaacaagagagtagtgtacgaagcgccgtttcgctc 1021
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 869 GCAAGAAAGGGAGCCTTCACACAGAGCTGCCCGCAGGAGACCTTAAGCGAGACTGCGCA 928
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QY 1022 agaacacacatgttatccagatgacatccaicaaagaacgaagatcccccagatgagatgaac 1081
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DB 929 ACNACAC-----CAGCTCTCTCCCGACGCAAGAAAGAAACCATGTGATGGAGAAAT 979
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QY 1082 tgttatacttaccagagagagcggtgagagactaagaatgctgttgaagaatacaagaagt 1141
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DB 980 ATTTCACCTTGTAGATCCGTGGGGCTGAGGCGCTTCGAGATGTTCCGAGAGCTGAATGAGG 1039
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QY 1142 cccctgaactcatgacagtaactccctccagca 1172
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DB 1040 CCTTGGAACTCAAGATGCCAGGCTGGGAA 1070
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```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,009
FILING DATE: 19-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommet, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
TELEX: 425066CURTMS
INFORMATION FOR SEQ. ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 1182 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-184-009-215

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Query Match 18.1%; Score 242.6; DB 2; Length 1182;
 Best Local Similarity 58.2%; Pred. No. 1.7e-63;
 Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

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QY 362 ctccatcacccgcacatccctcccaacacagcagcagcccgacagtttcgaagtg 421
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DB 275 CCTGTGATCTTCTGTCCTTCCAGAAAACCTACAGAGGACCTGCTGCTGCTG 334
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 422 ccttccagcagtcgagacacacgaagtcgccccttggaagttatccacgaactgaaga 481
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DB 335 GCTTCTTGCACTTGTGGAGACGCCAAGTCTGTGACTTGACAGTACTGCTCCCTCAACA 394
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 482 aactctactgccaatgtgcaaaagacatgcccacatcaagatgtagtgaacccacac 541
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 395 AGATGTTTTCAGCACTGAGCCAGACCTGCTGAGAGTGTGGTGTGATTCACACACCC 454
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QY 542 ctcaagagagctgtatccgagcagtcgctgtctacaaaagctgagcagtgagcagagag 601
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 455 CGCCCGGACCCCGCTCCGCGCATGCGCTACAGAGCTACAGACATGACAGAGG 514
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 602 tggtagagcgtgtcccaacacagtcgagcgtgaattcaacagagagacagattgccc 661
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DB 515 TTCTGAGGCGCTGCTCCCGACATGAGCGCTGCTACATGACGATG-----GTCTGCGCC 568
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QY 662 ctctcagtcattgtatctgagtagagagagacagcagtcagtcagtagaagatccca 721
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 569 CTCCTCAGCATCTTATCCGAGTGGAGAAATTTGCGTGTGAGATTTTGGATGACAGAA 628
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 722 tcaagagagagagagtagtgcgtgtaacctatgagacaccccgagttgagcagatga 781
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 629 ACACCTTTTGACACTATGCTGTGTGCTGCTGCTACAGAGCTACAGACATGACAGAGG 688
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 782 cgcagagctctgtacaattatcatgtgtaacagcagttgtgttgagagagatgaacgcgctgc 841
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 689 CCACCATTCACATCACTACATGTGTACAGTTCCTGCAATGCGCGCATGACCGGAGGC 748
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 842 caatttaattcatgttactctgtgaaacacagagatgagcagtcgtgagcgcagcgtgc 901
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 749 CCATCTCACCATCACTACACTGGAAGACTGCAGTGTATATCTACGTGGAGCAACGCT 808
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Patent No 5843654
GENERAL INFORMATION:
APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
APPLICANT: OLDENBURG, MARY C.
APPLICANT: HEISLER, LAURA
TITLE OF INVENTION: DETECTION OF P53 MUTATIONS
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,956
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,601
FILING DATE: 09-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,164
FILING DATE: 09-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL J, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FORS-01801
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 1182 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-484-956-94

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Query Match	18.1%	Score 242.6	DB 2	Length 1182
Best Local Similarity	58.2%	Pred. No. 1.7e-63		
Matches 472	Conservative 0	Mismatches 324	Indels 15	Gaps 2
OY	362	ctccatcacccgcgcatccctcccaacaccgagatcccaagcccgccgacagatttcgacgtt	421	
Db	275	ccctgctatcttctgtctccctcccgaaaccttaccagggcagctacgttccctctgg	334	
OY	422	cccttcagcagtcgagcacgcgccaagtctgcgcacctgtgacgtatccatctgaactga	481	
Db	335	gccttcttcattctggggacagcccaagctgtgacattggacagcaactccctgcctc	394	
OY	482	aaccttactgcgaattgcgaagacatgcccattcccaatcaagttgatgacccacctc	541	
Db	395	agatggttttggccaactggcccaagacctccctgtgcacctgtgggttgattccacaccc	454	

OY	542	ctcgggagcgtgtatccgcgcgcattccctggtctacaaaaaaagctgagcaagcgtccagagag	601
Db	455	CGCCCGGACCCGGCGTCCGGCCATGGCCATTCTACAGCAAGTCACAGACATGAGGGAGG	514
OY	602	tggtgaagcgggtgcgcccaacatgaaactgaagccgttgatctcaacagaggaacagatctgcc	661
Db	515	TTGTGAGGGCGGTGGCCCCACCATGATGAGGGCGTCTCAGATGAGCATG-----CTGTGGCCCC	568
OY	662	ctcctagtcaatttgattcggagttagaggggaaacagcattgccagtatgtagaagaatccca	721
Db	569	CTCCTCAGCACTCTTATCCGAGTGAAGGAATAATTTGGTGTGGAGATTTGGATGTGACAGAA	628
OY	722	tcaagagaagaacagagtgctgtgtgtaacctatgagccaccgccaggtttgcactgattacca	781
Db	629	ACACTTTTTCGACATAGT	688
OY	782	cgacagctctgttacaattcatgtgttaacagcaagctgtgttgtagaggaatgaaacgcgcgt	841
Db	689	CCACCATTCACATACACTACATCATGTGTATGATGTTCTCGATGGGGCGGACATGAACCGGAGAC	748
OY	842	caatttaatcatctgttacctctgtgaaacccagagatggtggaaatcctctgggccgagctgct	901
Db	749	CCATCTCTCACCATTATCATCACTGTAAGACCTCCAGTGTATCTACTGGGACCGGAACACTT	808
OY	902	ttgtagccccgagatctgtgctctgccagaagaacagagacggagtgaagatacaca	961
Db	809	TTTGAGTGTGCGT	868
OY	962	gaaagcagcaagttctcgagacagtaaaaaagacggtgatatgtgtcgaagcgcccgcttgctc	1021
Db	869	GCAAGAAAGGGGAGCCTTCACACAGAGTGGCCCCCAGGAGGACACTTAAGCAGGACACGCCCA	928
OY	1022	agaacaacacatgatatccagatgacatccatcaagaagaagaagatctcccaagatagtatgac	1081
Db	929	ACAAAC-----CAGTCTCTTCCCACGCAAGAAAGAAACCATCTGATGAGAAAT	979
OY	1082	tgtatacttaaccagltgaggggcccgtgagactatgaaatgcctgtgaaatcaaaagct	1141
Db	980	ATTTCACCCCTTCATATCCGTGGGGCGTAGCGGCTTCAGATGTTCCGAGAGCTGATGTAGG	1039
OY	1142	ccccggaactatgtcagttactctccacaga	1172
Db	1040	CTTTGAGACTTAAGATGCCACGAGCTGGGAA	1070

RESULT 12
; Sequence 92, Application US/08757653
; Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757, 653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.
 REGISTRATION NUMBER: 40,027
 REFERENCE/DOCKET NUMBER: FORS-02565
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1182 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-757-653-92

Query Match 18.1%; Score 242.6; DB 2; Length 1182;
 Best Local Similarity 58.2%; Pred. No. 1.7e-63;
 Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

QY 362 ctccatcaccgcacatccctcccaacacgcagcccgacaggttcgaagtg 421
 DB 275 CCCGTGATCTTGTGCTCCCTTCCAGAAACCTACCGAGCTACGGTTTCCGTG 334
 QY 422 ccttcacagcgtcagacacccgcaagtcggccacctggacgtatccactgaactgaaga 481
 DB 335 GCTTCTTGACATTTGGGACAGCCAGCTGTGTGACAGTACTCCCTCCCTCACA 394
 QY 482 aactctactcacaattgcaagacatgccccatccatcagatcaagtgatgacccacctc 541
 DB 395 AGATGTTTTCACACAGTGGCAACACCTGCTGCAAGCTGTGGTGTGATTTCCACACCC 454
 QY 542 ctcaaggagcgttctatccgcgcgcgtctgtctcaaaaaagcttgacacgctcagagag 601
 DB 455 CGCCCGGACCCCGTCCGCGCATGATCAACAGCATGACACATGACGAGG 514
 QY 602 tggtagagcgttcgcccaacatgagctgagccgtgaattcaacgagggagacagattggcc 661
 DB 515 TTGTGAGGCGCTCCCGCACATGAGCGCTGCAATGACGATG-----GTCCTGCGCC 568
 QY 662 ctctcagtcatttgatcagtagagaggaacagcagtcgccagttgtgagaagatccca 721
 DB 569 CTCCTCAGCATCTTATCCGAGTGAAGAAATTTGCTGTGGAGTATTGGATGACAGAA 628
 QY 722 tcaacgaggaacagagtgctgtgtacactatgagccaccccgattggcactgaattca 781
 DB 629 ACACCTTTGACATAGTGTGTGTGCTCCATGAGCGCGCTGAGTTGCTGTGACTGTA 688
 QY 782 cgcacgctctgtacaaattcatgtgtgtaacagcagttgtgtgagggatgaaccgcgtc 841
 DB 689 CCACCTCAGCATACACATGATGTGTGATGAGTCTGCAATGGCGGCAATGAACCGGAGGC 748
 QY 842 caatttaacatctgttactctggaacacagagatggaagtcctcggcgcaagcgtgtc 901
 DB 749 CCATCTCAGCATACATGAGTGAAGTCCAGTGTGATATCTACAGGAGCGGAACAGT 808
 QY 902 ttgagggccggagtgctgtgttcgccaggaagagacaggaagcgagatgaagatagcata 961
 DB 809 TTGAGGTGCTGTGTGTGTGCTGCTGAGAGACCGGCGCACAGGAGGAAGAAATCTCC 868
 QY 962 gaaagagaagaatttcgcgcagtagacaagaacggtgattcgcgaagcccggttcgtc 1021
 DB 869 GCAAGAAAGGGGAGCTCAGCAACAGAGCTCCCGGAGGAGCACTAAGCAGACTGCCCCA 928
 QY 1022 aagaacacacatggtatccagatgaatccatcaagaagaacagatccccaaga tgaaga 1081
 DB 929 ACACAC-----CAAGCTCTCTCCCGACCAAGAAAGAAACACATGATGAGAT 979
 QY 1082 tgttacttaccagtgagggcggtgagactatgaatgtctgtgaagaatcaagagat 1141
 DB 980 ATTTCACCTTATAGATCCCTGGGCGGTGAGCGCTTGAGATGTTCCAGAGACTGAATGAGG 1039
 QY 1142 ccttgaaactatcagtagtactctctcaagca 1172

DB 1040 CCTTGAACCTACAGATGCCCGAGCTGGAA 1070

RESULT 13
 US-08-757-653-94

; Sequence 94, Application US/08757653
 ; Patent No. 5843669
 GENERAL INFORMATION:
 APPLICANT: Kaiser, Michael W.
 APPLICANT: Lyamichev, Victor I.
 APPLICANT: Lyamichev, Natasha
 TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
 NUMBER OF SEQUENCES: 190
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Medlen & Carroll, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: California
 COUNTRY: United States Of America
 ZIP: 94104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/757,653
 FILING DATE:
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Ingolia, Diane E.
 REGISTRATION NUMBER: 40,027
 REFERENCE/DOCKET NUMBER: FORS-02565
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 94:
 SEQUENCE CHARACTERISTICS:

LENGTH: 1182 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-757-653-94

Query Match 18.1%; Score 242.6; DB 2; Length 1182;
 Best Local Similarity 58.2%; Pred. No. 1.7e-63;
 Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

QY 362 ctccatcaccgcacatccctcccaacacgcagcccgacaggttcgaagtg 421
 DB 275 CCCGTGATCTTGTGCTCCCTTCCAGAAACCTACCGAGCTACGGTTTCCGTG 334
 QY 422 ccttcacagcgtcagacacccgcaagtcggccacctggacgtatccactgaactgaaga 481
 DB 335 GCTTCTTGACATTTGGGACAGCCAGCTGTGTGACAGTACTCCCTCCCTCACA 394
 QY 482 aactctactcacaattgcaagacatgccccatccatcagatcaagtgatgacccacctc 541
 DB 395 AGATGTTTTCACACAGTGGCAACACCTGCTGCAAGCTGTGGTGTGATTTCCACACCC 454
 QY 542 ctcaaggagcgttctatccgcgcacgtctgtctcaaaaaagcttgagacagtgcaagg 601
 DB 455 CGCCCGGACCCCGGTCCCGCATGAGCTACACACATGACAGCAATGAGAGG 514
 QY 602 tggtagagcgttcgcccaacatgagctgagccgtggaattcaacgaggaagaattggcc 661
 DB 515 TTGTGAGGCGCTCCCGCACATGAGCGCTGCTCAGATGAGGATG-----GTCCTGCGCC 568
 QY 662 ctctcagtcatttgatcagtagaggggaacagcagtcgccagtatgtagaagatccca 721


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; Sequence 46, Application US/08796101
; Patent No. 6183752
; GENERAL INFORMATION:
; APPLICANT: EPSTEIN, STEPHEN E.
; APPLICANT: FINKEL, TOREN
; APPLICANT: SPEIR, EDITH
; APPLICANT: ZHOU, YI FU
; APPLICANT: ZHU, JIANHUI
; APPLICANT: ERDLE, LORNE
; APPLICANT: PINCUS, STEVEN
; TITLE OF INVENTION: RESTENOSIS/ATHEROSCLEROSIS DIAGNOSIS,
; TITLE OF INVENTION: PROPHYLAXIS AND THERAPY
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,101
; FILING DATE: 05-FEB-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: KOMALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 764-5574
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1182 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-796-101-46
```

```
Query Match      18.1%; Score 242.6; DB 4; Length 1182;
Best Local Similarity 58.2%; Pred. No. 1.7e-63;
Matches 472; Conservative 0; Mismatches 324; Indels 15; Gaps 2;

QY 362 ctccataccgcgcacccctcccaacacgcgactaccacgagccgcgcacagtctgaagtcgt 421
Db 275 CCTGTGTCATCTCTGTGTCCTTCCAGAAAACCTACCAAGGACACTACGGTTTCCTGTGG 334
QY 422 ccttcagcgagtcgagacgcgcgaagtcggcaactggaactgtatccactgaactgaaga 481
Db 335 GCTTCTTGCAATTGTGGAGACAGCCAACTGTGTGACTTGACAGTACTCCCTGCCCTCAACA 394
QY 482 aacttactctccaattgcaagaagacatgcccacatccagatcaagtgatgacccacctc 541
Db 395 AGATGTTTGGCAACTGGCCAAAGCTGCTGTGCAAGCTGTGGGTGATTCCACACACCC 454
QY 542 ctcaaggagctgtatccgcgcgcacatgctgtctacaaaagctgacacgctcagcagagg 601
Db 455 CGCCCGGACCCCGCTCGCGCCATGGCCATGTACAGAGCAATGACATGACGAGG 514
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Db 515 TTGTGAGGCGCTGCCCCCAATGAGCGCTGCTCAGATAGCGATG-----GTCTGGCCC 568
QY 662 ctccatgacttgaattcagagtagaggaagacagcattgtaagaagatccca 721
Db 569 CTCCTCAGCATCTTATCCAGAGTGAAGAAATTTCGTGTGAGATATTGATGATGACAGAA 628
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QY 722 tcacaggaagacagagtgctgtgttaccttatgagccaccagttgagacgaattca 781
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QY 1022 agaacacacatggtatccagatgacatccatcaagaagaagatcccgatgataac 1081
Db 929 ACAACAC-----CAGCTCTCTCTCCACAGCAAAAGAAACCTGATGGAGAA 979
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Db 980 AATTTCACCTTCAGATCCGTGGGCGTGAGCGCTTCGAGATGTTCCGAGACGTGAATGAGG 1039
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Db 1040 CCTGGAACCTCAAGATGCCCAAGCTGGGAA 1070
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Search completed: August 10, 2001, 00:39:37
Job time: 4060 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 9, 2001, 23:30:41 ; Search time 1394.72 Seconds
(without alignments)
9109.094 Million cell updates/sec

Title: US-09-670-568b-2_COPY_145_1488
Perfect score: 1344
Sequence: 1 atgtccagagcacacagac.....caaacgatacgtatacca 1344

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml?d12t1-dw3-c7-3-pw3-wr016>)

Seq primer: PUC 18 forward
081099-001-d01&t3=1999-10-08&t4=1)
P.L.C.I-FM&C2=PM2-H1U190

High quality sequence data

High quality sequence stop: 514

Location/Qualifiers

1

/organism="Homo sapiens"

/db_xref="taxon:9606"

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/clone 1fh="HT0190"
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/dev stage="Adult"

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/proc_cage null
/note="Organ: head

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LOW stringency conditions, "

ORIGINAL

COM
TENTIVE

Source:

1. .517

/organism="Homo sapiens"

/db_xref="taxon:960

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/clone_lib="HT0322"
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/dev stage="Adult"
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    /note="Organ: head neck: rest of head"

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ORIGIN

3
2
1

ORIGIN

Query Match

Best Local Similarity: 34.76; score 467; DB 115; Length 517

Matches 506; Correlation 95.7%; Pred. No. 2.7e-121

536 caaccctcccaaggagctcgttcaatccgcacatgctctctcaaaaaaagtctgacagctca 595
1 CAACCTCCTCGGAGCTGTATTCCGCCCATGCTCTTCAAAAAAGCTGACACGCA 60
596 cggaggtggtgaagcggctgccecaacacatgaagctgaagccgtgaattcaacagagacaga 655
61 CGGAGGTGTTGAACCGGTGGCCCAACCATGAGCTGAGCGCGTGAATTCAACGAGGACAGA 120
656 ttgcacctctcaatcattatctcgatgagggaggaagccatctgccatctatagaag 715
121 TTGCCCTCCTAGTCATTTGATTTGAGTGTGAGAGGGAACGCGCATGCCCATGTATTAAAG 180
716 atcccatcaagaagaacagagtgctgtgtaaccttaatgaagccaacccaggtttgacatg 775
181 ATCCCATCACAGGAACACAGAGTGTGCTGTACCTTATGAGCACCCAGTTTGCACTG 240
776 aattcacagacagctctgtac -aattcaatgttaacagcagttgtttgagagatgaac 834
241 AATTCAACGACAGCTTTGTACAAATTTCAATGTGTAAACACACTTGTGTAGAGGAGATGAAC 300
835 cgcgcgtcaatttaatcatgttactcttgaacaacaaagaattgacgaagctcctgggcgca 894
301 CGCGCTGCACAAATTTTATCATTTGTACTCTGTGAACACAGAGATGGGCAAGTCTGGGCCCA 360
895 cgcgtggttgaagcccgagatctgtgcttgcacagaagaacagagaagcggaatgaagat 954
361 CGCTGCTTTGAAGCCCGGATCTGTGCTTTGCCACAGAGAGACAGGAAGGGGATGAAGAT 420
955 agcatcaagaacacaaagtttcgacagctacaaagaacgtgatacgaagcgccg 1014

Db 421 AGCATGAGAAAGCAGCAAGTTTCGGACATGACAAAGAACGGTGTATG-----CG 468

QY 1015 ttccgtcagaacacacatggtatccagatgacatcatcacaagaagaa 1063
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Db 469 TTTCGTGACGAAACACACTATGTATCCAGATGACATCCATCAAGAAACGAA 517

RESULT 7
BF774398 450 bp mRNA EST 12-JAN-2001
LOCUS BF774398
DEFINITION 284057 MARC 3BOV Bos taurus CDNA 5', mRNA sequence.
ACCESSION BF774398
VERSION BF774398.1 GI:12122298
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 450)
Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrrentkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid,
W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
JOURNAL
COMMENT
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross-match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCGCCAGTCACGACG
Plate: 83 Row: C Column: 20
Seq primer: ATTAGTGACACTATAG.
Location/Qualifiers
1. 450
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
BASE COUNT 130 a 122 c 113 g 85 t
ORIGIN

Query Match 30.4%; Score 408.4; DB 169; Length 450;
Best Local Similarity 94.2%; Pred. No. 1e-104;
Matches 424; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 876 tgggcaagctctggcgcaagctgcttggagcccgcatctgcttggcccaagaaga 935
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Db 1 TGGGCAAGCTCTTG6GCGCGCTGCTTTGAGCCCGGATCTGtcttggcccaagaaga 60

QY 936 caggaagcgagatgaatgacatcagaagaagcagagtttcgagacagtaacaagaagc 995
|||||
Db 61 CAGGAAGCGCGATGAAGATGACATCAGAAAGCAGAGTCTCGGACAGCAAAAGATG 120

QY 996 tgaatgtaagaagcgccgcttgcgcagaacacacatgcatcagatgacatcatcaa 1055
|||||
Db 121 TGATGTACCAAGCGCGCTTCCGTCAAGAACACATGCGATCCAGATGACATCCATCAA 180

QY 1056 gaacgaagatccccaatgataacttatacttccagtgagggcgctgagattta 1115
|||||

Db 181 GAAGAAGATCCCGACATGATGATTAATACTTACAGTAAGGGCGGTGAGACTTA 240

QY 1116 tgaatgcttltgaagatcaaagagtccttggaaactatgacgtaccttctcagcaac 1175
|||||
Db 241 CGAATATCTGTGTAAGATCAAAAGATCCCTGGAACTCATGACATCTTCTCGACAC 300

QY 1176 aattgaagctacagcagaacagcagcagcagcagcagcagcagcagcagcagcagc 1215
|||||
Db 301 GATTGAACCTTACAGGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 360

QY 1236 ccttcagccttctcagaatgagctgtggaagcccgagagagaactccaacaac 1295
|||||
Db 361 CTTTCAAGCGCTGCTTCAAGATGAGCTTGTGAGACCGCGGAGAGAAACCCGAGACATC 420

QY 1296 tgaagcttcttagacattccaagcccc 1325
|||||
Db 421 TGACGCGCTTCTTGAACATTCAGTCCGCC 450

RESULT 8
AW379296 508 bp mRNA EST 04-FEB-2000
LOCUS AW379296
DEFINITION MR0-HT0241-091299-004-b02 HT0241 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW379296
VERSION AW379296.1 GI:6883955
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 508)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
JOURNAL
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR0&l2=MR0-HT0241-
091299-004-b02&l3=1999-12-09&l4=1)
Seq primer: puc 18 forward
High quality sequence start: 72
High quality sequence stop: 438.
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1. 508
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0241"
/dev_stage="adult"
/note="Organ: head,neck; Vector: puc18; Site.1: SmaI;
Site.2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
BASE COUNT 154 a 116 c 131 g 107 t
ORIGIN

Query Match 30.2%; Score 405.6; DB 115; Length 508;
Best Local Similarity 93.3%; Pred. No. 6.7e-104;
Matches 446; Conservative 0; Mismatches 29; Indels 3; Gaps 2;

QY 758 caccacagttggcagcgaattcagacagctctgtcaaat--tcattgttaacaagcag 815
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/clone_id="HT0241"
/dev_stage="Adult"
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site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 136,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

Kakuchi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishibe, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,

	Query Match Best Local Similarity Matches 464; Conservative	27.1%; 92.8%; 0;	Score 364.4; Pred. No. 3.2e-92; Mismatches 16;	DB 115; Indels 20;	Length 507; Gaps 77;
QY	572	tctacaaaaagctgagcagcgtctacaggaagtgtgtaaagcgggtgcccacatgaagctga			
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QY	632	gcgcgtgaattcaacgaaggagacagatctgcgcccccgctgcatcttgatcttgaggaagga			
DB	80	GCGCTGATTTCAACAGGAGGACAGATGTGCCCTCCCTAGTCATTGATTCAGATGAGGGGA			139
QY	692	acagacgatgccacgatctgtagaagaatcccatccacagaagaagaagaagatgtgcgtgtaacct			
DB	140	ACAGGCATGCCACGATGATGTAGAAGATCCCATACAGBAACACAGAGTGTGCTGTAACCTT			751
QY	752	atlaagcaccaccaggtctggcacctgaattc-accgaacgctctgttac-aatttcattgtcaa			
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OY	810	cagcaatctgtctgtgaaggaatgaacccgcgcctcaattatcatcttactc--ggaa	867
Db	260	CAGCAGTGTGTGTGAGGGATGAACCGCCGTCACATTTTAATCATGTGTACTCTTGAAA	319
OY	868	accagaatgtggcaatctctgtgcgcgaagctgcctttagagcccgatctgtctgccca	927
Db	320	ACCAAGAGATGGCAAGTCTCTGGAGCAGACGCTGCTAAAGAGCCCGGATCTGTGCTGCCCA	379
OY	928	ggaagag--acagaagcgcggaatgaagatagcatcagaagaagcaagtttcgacagta	985
Db	380	GGAAGAGACACAGCAGCAGCGGATCAAGATATACATCAGAAAGCAGCAGCTTCGACAGTA	439
OY	986	c-aagaacagtttagttagaagagcgccgtttcttgagaa--cacacatgataccagat	1043
Db	440	CAAAAGAACGTTGATG-----CGTATCTCGTAGAACACACACATGTATCCAGAT	487
OY	1044	gacatccatccaagaacgaa	1063
Db	488	GACATCCATCAAGAACGAA	507
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VERSION	BE752074.1	GI:10160066	
KEYWORDS	EST.		
SOURCE	cow.		
ORGANISM	Bos taurus		
REFERENCE	Elkayvoti; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos. 1 (bases 1 to 541) Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Fahrnkruyng,S.C., Freking,B.A., Rohrer,G.A., Laegreid ,M.W. and Keeler,J.W. Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle Unpublished (2000) Contact: Smith TP, USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smithm@mail.marc.usda.gov Single pass sequencing. Bases called and alt.trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options. PCR primers FORWARD: AGCAACAGCTATGACCAT BACKWARD: GTTTCACATCACGACG Plate: 45 row: M column: 16 Seq primer: ATTAGCTGACACTATG. Location/Qualifiers 1..541 /organism="Bos taurus" /db_xref="taxon:9913" /clone_id="MARC 2Bov" /tissue_type="pooled" /lab_host="DH10B" /note="Vector: pCMV SPORT6; Site.1: XbaI; Site.2: XhoI; library made from pooled tissue from testis, thymus, semilendonsus muscle, longissimus muscle, pancreas, adrenal, and endometrium."		
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BASE COUNT	149 a	132 c	133 g
ORIGIN			127 t
Query Match	27.0%	Score 363:	DB 139; Length 541;
Best Local Similarity	93.8%	Pred. No. 8.1e-92;	
Matches 378;	Conservative	0; Mismatches 25;	Indels 0; Gaps 0;

OY	942	gggagataaagaatagcatcacaanaacgaagaatttcgcgaacagttaaaaagacgtgatcg	1001
Db	1	GGCGGATGAAGTACATCAGAAAGCACAGGTCTTCGGACAGCACAAAAGATGTCATGG	60
OY	1002	tacgaagcgcccgcttctgcagaaacacacatgylatccagatgatcatcatcaagaacg	1061
Db	61	TACGAAGGCCCTTTCCGTCAGAACACACATGGCATTCAGATGACATCATCAAGAAACG	120
OY	1062	aagatcccagaatgtgaactgltacttaccagtgaggcgctgtagacttatgaaat	1121
Db	121	AAGATCCCCACATGATGTAAGTACTGTTACTTACCAAGTAAGGGCCCTGTAGACTTACGAAT	180
OY	1122	gctgttgaagttcaaagaagtcctctgaaactaatgtgaftaccttcttcagacaacattga	1181
Db	181	GCTGCTGAAGATCAAGAATCCCTTGAACTCATGTGCATGATCTTCTTACACACATTTGA	240
OY	1182	aacgtacaggaacaacgaacacgacgacgacacgacttacttcagaacacatctcttc	1241
Db	241	AACGTACAGGCGACGACGACAACACACACACAGCATTTACTTTCAGAAACATCTCCTTTC	300
OY	1242	agcctgtcttcaggaatgagctgtgtgagccccgagagagaactccaacaatctgaagt	1301
Db	301	AGCGCTTTCAGGAATGAGCTTGTGGACC CGGGGAGAAAAACCCGAGACAATCTGACGC	360
OY	1302	ctctcttagacatctccaaagcccccacacgactcagtgatcacca	1344
Db	361	CTTCTTAGACATTCAGATCCCCCAAATCGATCATGTATCCCA	403
RESULT	14		
LOCUS	BF303874	595 bp	mRNA
DEFINITION	60188668F12 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120604	EST	21-NOV-2000
VERSION	BF303874		
KEYWORDS	BF303874.1 GI:11250551		
SOURCE	EST.		
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
JOURNAL	1 (bases 1 to 595)		
COMMENT	NIH-MGC http://mgs.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-femail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.nsl.gov Plate: LNCMI001 row: a column: 21 High quality sequence stop: 595. Location/Qualifiers 1..595 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4120604" /clone_1lb="NIH_MGC_17" /tissue_type="fibroblastsarcoma" /lab_host="DH10B (phage-resistant)" /note="Organ: muscle; Vector: pOT97; Site_1: EcoRI; Site_2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." (Stratagene) and Superscript II RT (Life Technologies)." (Stratagene)		
BASE COUNT	129 a	206 c	157 g
			103 t

